

Supplementary Table 1: Differentially expressed genes in microarray with FDR<0.15 and q-PCR validation.

Rap1^{Δ/Δ}-LT-Cre vs. Rap1^{+/+}-LT-Cre

gene symbol	logFC	FDR	q-PCR Fold change ± SD
<i>Terf2ip</i>	-3.48	0.01	-261.3 ± 43.7
<i>Epb4.114a</i>	-4.72	0.04	-174.9 ± 32.0
<i>Slit3</i>	-3.33	0.056	-13.6 ± 0.8
<i>Stmn2</i>	+3.24	0.06	+18.2 ± 4.4
<i>Gria3</i>	-2.66	0.061	-66.6 ± 51.1
<i>Smtnl2</i>	-2.58	0.068	-5.2 ± 1.4
<i>Ifi27</i>	-3.4	0.068	-39.4 ± 32.7
<i>Nudt6</i>	-3.38	0.068	-7.2 ± 2.5
<i>Ctgf</i>	-2.82	0.068	-15.8 ± 4.8
<i>Car6</i>	-3.0	0.068	-34.5 ± 22.1
<i>Hs3st1</i>	-2.69	0.077	-12.4 ± 0.9
<i>Nnmt</i>	-3.96	0.077	-27.9 ± 19.9
<i>H19</i>	-3.57	0.09	-60.5 ± 15.0
<i>Adra2</i>	-2.1	0.1	-13.9 ± 0.2
<i>Gm12824</i>	-2.2	0.1	-8.9 ± 0.7
<i>Ened</i>	-2.35	0.12	-9.1 ± 0.7
<i>Igf2</i>	-2.64	0.3	-12.9 ± 0.5

Supplementary Table 2: Description of the differentially expressed genes (FDR<0.15) in wildtype versus *Rap1*-null MEFs.

type	NCBI Accesion	Gene symbol	Gene name	Cellular component	Function
Other	NP_065609	<i>Terf2ip, Rap1</i>	Terf2 interacting protein	Chromatin	Experimental control
Other	BAA05978	<i>Epb4.1I4a</i>	Erythrocyte protéina band 4.1-like factor	Unknown	Cell polarity, Proliferation Regulation of interaction between the cytoskeleton and plasma membrane. Component of β -catenin/TCF pathway
Other	AAD44760	<i>Slit3</i>	Slit homolog 3	Extracellular space	Cell motility Axonal guidance signaling <i>Slit1</i> orthologs are targets of Wnt/ β -catenin pathway
Other	NP_079561	<i>Stmn2</i>	Stathmin-like 2	Cytoplasm	Regulation of tubulin May play a role in neuronal differentiation, and in modulating membrane interaction with the cytoskeleton during neurite outgrowth
Ion channel	BAE06153	<i>Gria3</i>	Glutamate receptor, ionotropic, AMPA 3	Plasma membrane,	Glutamate signalling pathway Cell death, depolarization, neurotransmission, X-inactivation
Other	AK040279	<i>Ifi27</i>	Interferon, alpha-inducible proteína 27 like 2A	Unknown	Antigen presentation, inflammation, apoptosis
Growth factor	AAH27267	<i>Nudt6</i>	Nudix (Nucleoside diphosphate linked moiety X)-type motif 6	Extracellular space	Fibroblast growth factor; Wnt signalling
Growth factor	AAA37628	<i>Ctgf</i>	Connective tissue growth factor	Extracellular space	Cell adhesion, cell-matrix adhesion, cell growth, cell migration, receptor signaling pathway, cell differentiation, epidermis and lung development. IGF-1 signaling CTGF is a secreted protein known to modulate several growth factor-signaling pathways including TGF-beta, BMP, and Wnt
Enzyme	AAD12540	<i>Car6</i>	Carbonic anhydrase 6	Extracellular space	Nitrogen metabolism
Enzyme	AAB84387	<i>Hs3st1</i>	Heparan sulfate (glucosamine) 3-O-sulfotransferase 1	Cytoplasm	Cysteine metabolism, chondroitin sulfate and keratin sulfate biosynthesis
Enzyme	AAB94332	<i>Nnmt</i>	Nicotinamide N-methyltransferase	Cytoplasm	Cell migration, calorie restriction, cancer
Non-protein coding RNA	AK145379	<i>H19</i>	H19 fetal liver mRNA, imprinted maternally expressed transcript	Unknown	Proliferation, S phase, regulation of <i>Igf2</i>
G-protein coupled receptor	AAA37213	<i>Adra 2</i>	Adrenergic receptor, alpha 2a	Integral plasma membrane,	Aggregation, binding, shape change, proliferation, cell movement, cell death, morphology
Other	AAH56975	<i>Ened</i>	Expressed in nerve and epithelium	cytoplasm	Hypothetical protein
Other	CAM20425	<i>Gm12824</i>	Predicted gene 12824	Unknown	Hypothetical protein
Other	NP_808444	<i>Smntl2</i>	Smoothelin-like 2	Unknown	Calponin homology domain

Supplementary Table 3A. Gene set enrichment analysis (GSEA). Pathways overrepresented in *wildtype-LT-Cre* compared to *Rap1^{Δ/Δ}- LT-Cre* MEFs (FDR<25%)

Source	Pathway / Gene set	Description	FDR
http://www.genemania.org/site/genes-by-species.Mus+musculus	Imprinted genes		<10 ⁻⁴
KEGG	gap junction	Gap junctions contain intercellular channels that allow direct communication between the cytosolic compartments of adjacent cells	0.080
KEGG	Complement and coagulation cascade	Blood coagulation is a series of coordinated and calcium-dependent proenzyme-to-serine protease conversions likely to be localized on the surfaces of activated cells in vivo	0.047
KEGG	Neuroactive ligand-receptor interaction		0.085
KEGG	Cell adhesions molecules (CAMS)	Cell-matrix adhesions play essential roles in important biological processes including cell motility, cell proliferation, cell differentiation, regulation of gene expression and cell survival	0.082
KEGG	Long-term potentiation	Hippocampal long-term potentiation (LTP), a long-lasting increase in synaptic efficacy, is the molecular basis for learning and memory	0.070
KEGG	Retinol metabolism		0.097
KEGG	Nitrogen metabolism		0.104
KEGG	Focal adhesion	Cell-matrix adhesions play essential roles in important biological processes including cell motility, cell proliferation, cell differentiation, regulation of gene expression and cell survival.	0.101
KEGG	Calcium signalling pathway	The voltage-operated channels (VOCs) are found in excitable cells and generate the rapid Ca ²⁺ fluxes that control fast cellular processes.	0.096
KEGG	Nicotinate and nicotinamide metabolism		0.115
KEGG	Melanoma	Oncogenic NRAS mutations activate both effector pathways Raf-MEK-ERK and PI3K-Akt. The Raf-MEK-ERK pathway may also be activated via mutations in the BRAF gene. The PI3K-Akt pathway may be activated through loss or mutation of the inhibitory tumor suppressor gene PTEN. Moreover, melanoma development is strongly associated with inactivation of the p16INK4a/CDK4,6/pRb and p14ARF/HMD2/p53 tumor suppressor pathways. The vertical-growth phase and metastatic melanoma are notable for striking changes in the control of cell adhesion.	0.177
KEGG	Graft vs host disease	Graft-versus-host disease (GVHD) pathophysiology can be summarized in a three-step process: the conditioning regimen , donor T-cell activation and the effector phase	0.164
KEGG	PPAR signalling pathway	Peroxisome proliferator-activated receptors (PPARs) are nuclear hormone receptors that are activated by fatty acids and their derivatives. PPAR has three subtypes (PPARalpha, beta/delta, and gamma) showing different expression patterns in vertebrates. Each of them is encoded in a separate gene and binds fatty acids and eicosanoids. PPARalpha plays a role in the clearance of circulating or cellular lipids via the regulation of gene expression involved in lipid metabolism in liver and skeletal muscle. PPARbeta/delta is involved in lipid oxidation and cell proliferation. PPARgamma promotes adipocyte differentiation to enhance blood glucose uptake.	0.094

KEGG	MAPK signalling pathway	The mitogen-activated protein kinase (MAPK) cascade is a highly conserved module that is involved in various cellular functions, including cell proliferation, differentiation and migration. Mammals express at least four distinctly regulated groups of MAPKs, extracellular signal-related kinases (ERK)-1/2, Jun amino-terminal kinases (JNK1/2/3), p38 proteins (p38alpha/beta/gamma/delta) and ERK5, that are activated by specific MAPKKs: MEK1/2 for ERK1/2, MKK3/6 for the p38, MKK4/7 (JNKK1/2) for the JNKs, and MEK5 for ERK5. Each MAPKK, however, can be activated by more than one MAPKKK, increasing the complexity and diversity of MAPK signalling. Presumably each MAPKKK confers responsiveness to distinct stimuli. For example, activation of ERK1/2 by growth factors depends on the MAPKKK c-Raf, but other MAPKKKs may activate ERK1/2 in response to pro-inflammatory stimuli.	0.193
KEGG	Regulation of Actin Cytoskeleton		0.242
KEGG	Olfactory Transduction	Within the compact cilia of the olfactory receptor neurons (ORNs) a cascade of enzymatic activity transduces the binding of an odorant molecule to a receptor into an electrical signal that can be transmitted to the brain. Odorant molecules bind to a receptor protein (R) coupled to an olfactory specific Gs-protein (G) and activate a type III adenylyl cyclase (AC), increasing intracellular cAMP levels. cAMP targets an olfactory-specific cyclic-nucleotide gated ion channel (CNG), allowing cations, particularly Na and Ca, to flow down their electrochemical gradients into the cell, depolarizing the ORN. Furthermore, the Ca entering the cell is able to activate a Ca-activated Cl channel, which would allow Cl to flow out of the cell, thus further increasing the depolarization. Elevated intracellular Ca causes adaptation by at least two different molecular steps: inhibition of the activity of adenylyl cyclase via CAMKII-dependent phosphorylation and down-regulation of the affinity of the CNG channel to cAMP. Longer exposure to odorants can stimulate particulate guanylyl cyclase in cilia to produce cGMP and activate PKG, leading to a further increase in amount and duration of intracellular cAMP levels, which may serve to convert inactive forms of protein kinase A (PKA2) to active forms (PKA*). As part of a feedback loop, PKA can inhibit the activation of particulate guanylyl cyclase.	0.057
KEGG	Heparan sulfate biosynthesis		0.240
Biocarta	Sprouty regulation of tyrosine kinase signal (SPRY) pathway	Block the cellular proliferation and differentiation induced by several different growth factors, including EGF and FGF	0.118
Reactome	Peptide binding receptors	These receptors, a subset of the Class A/1 (Rhodopsin-like) family, all bind peptide ligands which include the chemokines, opioids and somatostatins.	0.128
Reactome	Regulation of Insulin Secretion	Pancreatic beta cells integrate signals from several metabolites and hormones to control the secretion of insulin. In general, glucose triggers insulin secretion while other factors can amplify or inhibit the amount of insulin secreted in response to glucose. Factors which increase insulin secretion include the incretin hormones Glucose-dependent insulinotropic polypeptide (GIP and glucagon-like peptide-1 (GLP-1), acetylcholine, and fatty acids. Factors which inhibit insulin secretion include adrenaline and noradrenaline.	0.106
Reactome	Class A/1 (Rhodopsine-like receptors)	They represent members which include hormone, light and neurotransmitter receptors and encompass a wide range of functions including many autocrine, paracrine and endocrine processes	0.080
Genmapp	Prostaglandin synthesis regulation		0.021
Genmapp	Porphyrin and chlorophyll metabolism		0.242
Genmapp	GPCRDB class rhodopsin like		0.239

Supplementary Table 3B. Gene set enrichment analysis (GSEA). Pathways overrepresented in *Rap1^{AA}- LT-Cre* compared to *wildtype-LT-Cre* MEFs (FDR<25%).

Source	Pathway / Gene set	Description	FDR
KEGG	Type II Diabetes Mellitus	Insulin resistance is strongly associated with type II diabetes. "Diabetogenic" factors including FFA, TNFalpha and cellular stress induce insulin resistance through inhibition of IRS1 functions. Serine/threonine phosphorylation, interaction with SOCS, regulation of the expression, modification of the cellular localization, and degradation represent the molecular mechanisms stimulated by them. Various kinases (ERK, JNK, IKKbeta, PKCzeta, PKCtheta and mTOR) are involved in this process.	0.067
KEGG	ABC transporters	The ATP-binding cassette (ABC) transporters form one of the largest known protein families, and are widespread in bacteria, archaea, and eukaryotes. They couple ATP hydrolysis to active transport of a wide variety of substrates such as ions, sugars, lipids, sterols, peptides, proteins, and drugs. The structure of a prokaryotic ABC transporter usually consists of three components; typically two integral membrane proteins each having six transmembrane segments, two peripheral proteins that bind and hydrolyze ATP, and a periplasmic (or lipoprotein) substrate-binding protein. Many of the genes for the three components form operons as in fact observed in many bacterial and archaeal genomes. On the other hand, in a typical eukaryotic ABC transporter, the membrane spanning protein and the ATP-binding protein are fused, forming a multi-domain protein with the membrane-spanning domain (MSD) and the nucleotide-binding domain (NBD)	0.216

Supplementary Table 4. Microarray experiment revealed 478 downregulated genes showing log fold-change < -1 in *Rap1*-null MEFs compared to wild-type MEFs. The table shows the complete list of the downregulated genes (619 probes in the array platform) ranked by logFC value. Genes highlighted in bold letters are those which were also found statistically significant (FDR<0.15). FDR: False Discovery Rate.

Probe ID	Gene Symbol	logFC KO/WT	FDR value
A_51_P513898	Epb4.1l4a	-4.723426669	0.039877259
A_51_P343689	Slc14a1	-4.074837904	0.460257271
A_52_P251690	Gvin1	-4.05595589	0.344839936
A_51_P476767	Nnmt	-3.961261028	0.077029893
A_52_P661713	Gvin1	-3.906559802	0.327198019
A_52_P381806	Terf2ip	-3.792881485	0.010134393
A_51_P220150	Angptl7	-3.752414018	0.174220562
A_51_P241068	Dkk2	-3.719033096	0.460257271
A_51_P142196	H19	-3.569548012	0.090620386
A_52_P571350	H19	-3.567602196	0.115961442
A_52_P381813	Terf2ip	-3.484467656	0.010134393
A_52_P90363	Ifi27	-3.460937415	0.07885379
A_51_P358233	Ifi27	-3.403319141	0.06864005
A_51_P255699	Mmp3	-3.395148262	0.299894481
A_52_P1067757	Nudt6	-3.380168635	0.06864005
A_51_P259296	Lpl	-3.379084882	0.424190715
A_51_P355765	Slit3	-3.333936717	0.056723592
A_51_P235945	Hp	-3.313051182	0.460257271
A_52_P90364	Ifi27	-3.301148289	0.068870388
A_51_P312336	Slc14a1	-3.209085856	0.460257271
A_52_P309381	Cfh	-3.206992745	0.460257271
A_51_P249286	Rgs16	-3.124803157	0.391225768
A_52_P592007	Tfp1	-3.122958982	0.274514107
A_52_P535484	Gvin1	-3.077015747	0.427872245
A_51_P334104	Dcn	-3.031471555	0.460257271

A_51_P196444	Foxc2	-2.986872548	0.229746026
A_52_P310511	Car6	-2.984250708	0.06864005
A_51_P426353	Ucp1	-2.977020534	0.460257271
A_52_P282058	Col8a1	-2.962964024	0.189772183
A_51_P408584	4833416E15Rik	-2.949055404	0.250025455
A_51_P102987	Penk1	-2.918621572	0.312740901
A_51_P301809		-2.867471194	0.06864005
A_51_P112308	1810011O10Rik	-2.842187974	0.460257271
A_51_P157042	Ctgf	-2.815849741	0.06864005
A_52_P292792	Col8a1	-2.768391349	0.246843214
A_51_P260312	4732435N03Rik	-2.741880107	0.152006106
A_52_P515247	Arhgdb	-2.708639821	0.441832396
A_51_P479715	Eif2s3y	-2.695572335	0.460257271
A_52_P431615	Gm1966	-2.68901344	0.438302037
A_51_P365152	Hs3st1	-2.685267187	0.077029893
A_52_P272364		-2.659117157	0.060609407
A_51_P516826	Igf2	-2.644036237	0.311019882
A_51_P400335	Terf2ip	-2.635227204	0.039877259
A_52_P286166	Penk1	-2.623338746	0.390412631
A_51_P336833	Fabp4	-2.611377931	0.250025455
A_52_P387009	Egln3	-2.604309102	0.41562769
A_52_P395149	D130058I21Rik	-2.582703655	0.06864005
A_52_P185907	Crabp1	-2.578964238	0.477247891
A_51_P336830	Fabp4	-2.569129446	0.260658057
A_52_P514407	Klra15	-2.556093362	0.460257271
A_51_P390967	Slc43a3	-2.54892002	0.189772183
A_51_P423518	Amph	-2.548656489	0.460257271
A_52_P562040	9330188P03Rik	-2.524745095	0.460257271
A_52_P479249	Thy1	-2.506967516	0.460257271
A_52_P265584	1810011O10Rik	-2.503827992	0.460257271
A_51_P262401	Itga6	-2.483593642	0.45908694

A_51_P192955		-2.482986273	0.217061842
A_52_P670263	Tfpi	-2.473013562	0.19497458
A_52_P38011	0710005M24Rik	-2.44863679	0.460257271
A_52_P257625	Esm1	-2.426817145	0.45199466
A_51_P516833	Igf2	-2.41614878	0.312740901
A_51_P337412	Efemp1	-2.393312929	0.269244551
A_52_P569375	Fgf5	-2.388474343	0.312740901
A_52_P482897	Areg	-2.386246779	0.460257271
A_51_P277336	Sdpr	-2.378389741	0.45199466
A_52_P248513	Klra7	-2.375926303	0.460257271
A_52_P111031	Pcdh17	-2.37473462	0.460257271
A_52_P481957	Grem1	-2.3735384	0.404912554
A_52_P376360	Pdgfc	-2.369343952	0.460257271
A_51_P496569	Slit2	-2.365527098	0.217061842
A_51_P511787	Casp4	-2.359809828	0.412853057
A_51_P125205	Aqp1	-2.353132426	0.200008697
A_51_P333839	Pdgfc	-2.352329323	0.460257271
A_51_P132079	Klra22	-2.351642951	0.460257271
A_51_P134228	Hlf	-2.349927949	0.336633834
A_51_P351896	1110032E23Rik	-2.346477808	0.121364321
A_51_P358765	Spp1	-2.341469658	0.460257271
A_51_P444447	Cebpd	-2.325273645	0.246843214
A_51_P246543	Ebf3	-2.313225125	0.460257271
A_51_P501844	Cyp26b1	-2.308309673	0.152006106
A_51_P496562	Slit2	-2.305927445	0.217061842
A_51_P345649	Pdgfra	-2.302999428	0.404912554
A_51_P392303	Lrrn3	-2.262540874	0.250025455
A_52_P636948	Pdgfd	-2.260429181	0.460257271
A_52_P479262	Col6a3	-2.252594654	0.252054211
A_51_P359272	Alcam	-2.244807355	0.178326111
A_52_P376574	Pcsk6	-2.212435026	0.460257271

A_52_P226664		-2.20751812	0.311019882
A_52_P796840	BC026782	-2.205891293	0.460257271
A_52_P727235		-2.189085565	0.103547631
A_51_P337308	Saa3	-2.17679609	0.493547225
A_52_P235347	Fgf21	-2.173975759	0.186823631
A_51_P213359	Has2	-2.159508377	0.460257271
A_52_P58145	Aldh1a2	-2.144792026	0.515387348
A_51_P375771	Ptchd1	-2.14146691	0.239911326
A_51_P490136	Spry1	-2.140612475	0.252054211
A_51_P309920	Itga8	-2.131300769	0.250025455
A_52_P120803	Ankrd1	-2.131081553	0.460257271
A_51_P394354	5730469M10Rik	-2.130691941	0.45311155
A_51_P411917	Gata6	-2.130003084	0.41562769
A_52_P197199		-2.123289847	0.460257271
A_52_P114889	Upk3b	-2.117968544	0.513019693
A_51_P137322	Cck	-2.109861748	0.460257271
A_51_P146560	Msln	-2.108397081	0.424190715
A_51_P434567	Adra2a	-2.094801584	0.103547631
A_52_P309389	Cfh	-2.083726045	0.460257271
A_51_P142972	Prdm8	-2.058210209	0.460257271
A_52_P669035	Clca1	-2.046512857	0.460257271
A_52_P81270	Itga6	-2.042615854	0.460257271
A_51_P387239	Iigp1	-2.028308731	0.438302037
A_52_P253179	Igfbp3	-2.022521955	0.465466098
A_51_P408343	Ifi204	-2.019572235	0.260658057
A_51_P355753	Hic1	-2.008204313	0.250025455
A_52_P342828	Fez1	-2.002242362	0.460257271
A_52_P257812	Lpl	-1.997630442	0.460257271
A_51_P185882	Ccdc68	-1.987790204	0.460257271
A_52_P145912	Mylk	-1.983285592	0.460257271
A_51_P451377	Kng1	-1.972181759	0.460257271

A_51_P324923	Man2a1	-1.971362566	0.189772183
A_51_P278334	Vldlr	-1.969415327	0.390412631
A_51_P408346	Ifi204	-1.961074302	0.317627182
A_51_P262515	Phf11	-1.952206777	0.415874965
A_51_P237856	Ifi203	-1.942156667	0.460257271
A_51_P432432	Pcdh9	-1.938229893	0.460257271
A_51_P188704	Unc13a	-1.933790215	0.441154035
A_51_P208793	C1s	-1.932051151	0.460257271
A_52_P11441	Rab6b	-1.924075217	0.229746026
A_51_P290065	Gap43	-1.916191271	0.460257271
A_51_P181772	Ptpre	-1.90808161	0.460257271
A_52_P209944	C130071C03Rik	-1.907140809	0.440547731
A_51_P180413	C130076O07Rik	-1.904465849	0.460257271
A_51_P344018	Klra13	-1.903790376	0.460257271
A_51_P101729	Cfh	-1.900172813	0.460257271
A_52_P264790	Pdgfd	-1.899610708	0.460257271
A_51_P398723	Flt1	-1.894708325	0.45199466
A_51_P331805	Kctd15	-1.887962859	0.460257271
A_51_P202408	Ptgir	-1.88513412	0.357073347
A_51_P268673	2210016H18Rik	-1.885124621	0.460257271
A_52_P322181	Adrb1	-1.880068476	0.206902621
A_52_P204311	Spry4	-1.868896903	0.269244551
A_51_P493234	Cp	-1.867923133	0.460257271
A_51_P338443	Angptl4	-1.860048383	0.460257271
A_51_P298741	Klra20	-1.857283317	0.460257271
A_51_P305583	Sp100	-1.853731938	0.322096565
A_51_P483324	Ptpn22	-1.839754993	0.460257271
A_52_P571537	3110039M20Rik	-1.839404219	0.460257271
A_51_P142744	Sulf1	-1.839242808	0.460257271
A_51_P262766	Ccnd1	-1.83781248	0.460257271
A_51_P309917	Itga8	-1.83708549	0.28367135

A_52_P568895	Kcb1	-1.825352263	0.460257271
A_52_P575217	Mylk	-1.813184558	0.404912554
A_51_P301804	St3gal1	-1.810781919	0.438302037
A_52_P288892	Klra12	-1.805602059	0.460257271
A_52_P121978		-1.789614559	0.460257271
A_52_P484194	Il1rl1	-1.783239192	0.460257271
A_52_P489232	Jph1	-1.779809148	0.311019882
A_51_P387591	Nfkbiz	-1.777357253	0.404912554
A_51_P334335	Isl2	-1.769829663	0.404912554
A_51_P376238	Serpingle1	-1.765303535	0.152006106
A_51_P129229	Ifi47	-1.760639529	0.264969446
A_51_P331570	Trib3	-1.760171474	0.252054211
A_52_P87839	Sema3c	-1.759086166	0.312740901
A_51_P240614	Tm4sf1	-1.755803171	0.460257271
A_52_P102846	Tcrb-V13	-1.751160366	0.441832396
A_51_P481693	Ero1l	-1.749666072	0.460257271
A_52_P39083	Ccbe1	-1.74441325	0.460257271
A_51_P134812	Chac1	-1.72826659	0.252054211
A_52_P570240	Kbtbd11	-1.727437834	0.299894481
A_51_P288876	Tmem45a	-1.723951151	0.290915985
A_51_P502614	Dusp6	-1.723648265	0.460257271
A_51_P284177	Akr1c14	-1.723417075	0.28367135
A_51_P475704	Pcdh9	-1.722755464	0.460257271
A_51_P324450	Pbp2	-1.718046209	0.461710604
A_51_P426270	Mgp	-1.717614064	0.260658057
A_52_P261184	Il1rl2	-1.713161256	0.460257271
A_51_P500044	Vldlr	-1.711508895	0.41562769
A_52_P600274	Trib3	-1.703295289	0.274514107
A_52_P283041	Smarca1	-1.695689348	0.460257271
A_52_P498193	Aldh1l2	-1.695114949	0.41562769
A_51_P381821	Fst	-1.693417226	0.228120205

A_51_P308362	Ugt1a6b	-1.691246899	0.460257271
A_52_P325527	Edil3	-1.691188324	0.461710604
A_52_P660648	Pla2g4a	-1.683763767	0.353179102
A_51_P428013	Eml2	-1.678932571	0.460257271
A_51_P402760	Pla2g4a	-1.678463905	0.311019882
A_52_P380369	D14Ert668e	-1.673859276	0.460257271
A_51_P503722	Elavl4	-1.672486708	0.460257271
A_51_P377620	Ifi205	-1.672259997	0.404912554
A_52_P63044	Lsp1	-1.667370641	0.404912554
A_51_P142421	Rspo1	-1.665554504	0.543992109
A_52_P67493	Adra2a	-1.663576347	0.312740901
A_51_P265571	Adm	-1.663027364	0.460257271
A_51_P484111	Matn2	-1.662519365	0.390412631
A_51_P437978	Agtr2	-1.660596152	0.460257271
A_52_P68261	Pde6h	-1.657570349	0.460257271
A_51_P281333	St3gal6	-1.652079564	0.460257271
A_51_P334942	Aldh1a1	-1.643498919	0.526037858
A_52_P619248	Mrpplf4	-1.642815564	0.471468476
A_51_P424868	Mid1ip1	-1.641547123	0.250025455
A_51_P366138	Mertk	-1.639111779	0.260658057
A_52_P646957	Grpr	-1.635112749	0.250025455
A_51_P384230	Sgk2	-1.634499599	0.45908694
A_51_P402994	Ddx3y	-1.625060733	0.404912554
A_51_P431737	Cth	-1.623661602	0.311019882
A_51_P268748	2610203C20Rik	-1.619377376	0.460257271
A_51_P432567	Foxg1	-1.617974933	0.460257271
A_51_P184484	Mmp13	-1.616840533	0.489195351
A_51_P303061	Adcy8	-1.615653707	0.460257271
A_52_P546363	Gata3	-1.60819607	0.466285286
A_52_P461777	Pcdh9	-1.607963082	0.460257271
A_52_P384100	Bdnf	-1.605057538	0.404912554

A_51_P355122	Tnni2	-1.604458231	0.438302037
A_51_P489192	Postn	-1.601091891	0.460257271
A_51_P243514	4732474015Rik	-1.597822162	0.460257271
A_51_P461404	Smarca1	-1.578739532	0.460257271
A_51_P503822	Slitrk6	-1.568318152	0.460257271
A_52_P631889	Tfpi	-1.56685232	0.327193678
A_51_P230382	Etv4	-1.561503367	0.460257271
A_51_P315925	Fgf21	-1.558118127	0.252054211
A_52_P619388	Kcnq1ot1	-1.55536773	0.460257271
A_51_P259603	Adcyap1r1	-1.551998414	0.493547225
A_51_P339793	I1rl1	-1.54704082	0.460257271
A_51_P223498	Slc39a10	-1.546637343	0.45199466
A_52_P418901	Evi1	-1.544533964	0.460257271
A_51_P380005	Galnt3	-1.542562069	0.460257271
A_52_P634218	C1s	-1.540771773	0.460257271
A_52_P599317	Hs6st2	-1.538979099	0.460257271
A_52_P507736	Itgb8	-1.53675125	0.438302037
A_52_P300730	Hmga2	-1.532368046	0.460257271
A_52_P86965		-1.531849496	0.398730577
A_51_P188114	Eps8	-1.531461083	0.460257271
A_52_P637573	Eif4g3	-1.529891728	0.404912554
A_52_P493502	Vps13a	-1.527871409	0.48562361
A_51_P382393	Errfi1	-1.527292354	0.404912554
A_51_P307979	Etv1	-1.523469389	0.4674057
A_51_P294643	Cdr2	-1.522358385	0.374791486
A_52_P1165070	Slco2a1	-1.522111507	0.250025455
A_52_P411780	Hdac9	-1.5210162	0.460257271
A_51_P265806	Clca2	-1.519459301	0.460257271
A_51_P291417	Thbd	-1.51646037	0.424190715
A_52_P145433	D7Erttd715e	-1.512849472	0.460257271
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A_51_P254855	Ptgs2	-1.501873735	0.460257271
A_51_P335000	Fhl1	-1.500310286	0.460257271
A_52_P319438	Ankr37	-1.499028087	0.461162735
A_51_P261991	Bdnf	-1.498750852	0.404912554
A_51_P420276	Plxdc2	-1.498600426	0.460257271
A_52_P615362	Flrt2	-1.498246263	0.446954216
A_51_P495780	S3-12	-1.495978658	0.460847823
A_52_P235319	Ptpre	-1.493022831	0.460257271
A_51_P166648	4931408A02Rik	-1.485048275	0.272546529
A_51_P430055	Tspan7	-1.484811626	0.460257271
A_51_P215475	Ptprb	-1.484685293	0.460257271
A_52_P333529	Slco2a1	-1.481654875	0.260658057
A_52_P379277	Enpp3	-1.475622981	0.424190715
A_52_P536494	Mycn	-1.462878429	0.473254072
A_51_P101347		-1.462551136	0.460257271
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A_51_P357606	Phyhd1	-1.456497477	0.460257271
A_51_P288406	Insl3	-1.45530835	0.460257271
A_51_P367720	Clu	-1.451632372	0.460257271
A_52_P229052	Tmeff2	-1.450608772	0.460257271
A_51_P379997	Galnt3	-1.446358455	0.460257271
A_51_P239750	Inhba	-1.442948492	0.460257271
A_52_P116006	Gda	-1.440782263	0.252054211
A_52_P497715		-1.43969781	0.460257271
A_52_P175157	Mef2a	-1.43818478	0.460257271
A_52_P6070	4931408A02Rik	-1.433907489	0.267413708
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A_52_P533673		-1.432991833	0.460257271
A_52_P603668	Aig1	-1.430951341	0.460257271
A_52_P442567	Trim30	-1.430261205	0.460257271

A_52_P224760	Ptgs2	-1.430072809	0.460257271
A_52_P633550	Ghr	-1.429648041	0.404912554
A_52_P368532	Spry2	-1.428376269	0.412853057
A_51_P185897		-1.427329696	0.460257271
A_51_P188111	Eps8	-1.426295131	0.460257271
A_51_P383001	Meox2	-1.426187944	0.460257271
A_51_P517075	Serpinf1	-1.424084822	0.460257271
A_51_P256170	Akr1c18	-1.415479507	0.390412631
A_52_P244736	Cxadr	-1.414319641	0.424190715
A_51_P139920	Mgll	-1.412055395	0.563059767
A_52_P35048	Serpinf1	-1.407180205	0.460257271
A_52_P633597	2310015N21Rik	-1.407137368	0.460257271
A_52_P265945	C330050A14Rik	-1.406735377	0.460257271
A_52_P21	Ttc9	-1.401657895	0.460257271
A_51_P509997	Cox6a2	-1.401228645	0.481646787
A_51_P193336	Nucb2	-1.401027574	0.454717208
A_51_P182303	Col1a2	-1.400515118	0.460257271
A_52_P84814	Plf2	-1.399685258	0.488180333
A_51_P508959	E130201N16Rik	-1.392215585	0.460257271
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A_52_P176245	Gata6	-1.385879327	0.460257271
A_51_P269546	Trem2	-1.384862383	0.267413708
A_51_P275454	Trim30	-1.38177039	0.460257271
A_52_P354744	Slc2a3	-1.380564304	0.460257271
A_51_P403536	Ltbp4	-1.380511571	0.460257271
A_51_P478172	Tcrb-V13	-1.378200102	0.460257271
A_51_P224843	Tmsb4x	-1.363118749	0.388292474
A_52_P220810	Trib2	-1.362751651	0.45199466
A_51_P276418	Rab6b	-1.360922801	0.440547731
A_51_P124254	Col4a1	-1.356997485	0.460257271

A_51_P185229	Bmp2	-1.356949953	0.460257271
A_51_P226016	Slc30a4	-1.356332158	0.460257271
A_51_P420731	Thy1	-1.354271862	0.460257271
A_52_P380263	Podxl	-1.352906718	0.460257271
A_52_P42269	Fgf10	-1.347038159	0.290915985
A_52_P139569	Mfap3l	-1.345084177	0.483760388
A_52_P199633	AI451617	-1.339572433	0.460257271
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A_52_P470663		-1.333749439	0.460257271
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A_51_P106799	Pparg	-1.330337646	0.460257271
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A_52_P476731	9030611O19Rik	-1.313927325	0.473562325
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A_52_P78423	5330421C15Rik	-1.303016049	0.456133767
A_52_P627327		-1.299661062	0.460257271
A_52_P604345	2610203C20Rik	-1.298432369	0.460257271
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A_51_P387608	Hif1a	-1.292413654	0.45199466
A_52_P679105	Prss23	-1.291592939	0.460257271
A_52_P78203	Acsl4	-1.290868831	0.460257271
A_51_P169061	Ayt1	-1.290566375	0.460257271
A_51_P306067	Lpp	-1.289898362	0.424190715
A_51_P157902	Cldn3	-1.288548264	0.460257271
A_52_P497188		-1.288233473	0.460257271
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A_52_P418515	1700007G11Rik	-1.28446706	0.460257271
A_52_P189970	Stc1	-1.282764274	0.460257271
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A_51_P277994	Oas2	-1.281931764	0.404912554
A_51_P413059	Mcpt8	-1.280608525	0.460257271
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A_51_P271665	Rev3l	-1.272817934	0.460257271
A_51_P253074	Chit1	-1.270482553	0.460257271
A_51_P362638	Trf	-1.264620271	0.561574461
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A_51_P396852	Gsto2	-1.263530564	0.452554737
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A_52_P676510	Tgtp	-1.260662244	0.460257271
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A_52_P59318	Rdh10	-1.259955732	0.460847823
A_52_P372901	Plscr2	-1.259282696	0.470177319

A_51_P212308	Cxadr	-1.256952369	0.440168683
A_51_P463003	Tslp	-1.256786039	0.441154035
A_52_P527800	Emilin2	-1.256317119	0.460257271
A_51_P394764	9030611O19Rik	-1.254542565	0.488088614
A_51_P452533	D1Ert471e	-1.253998644	0.609036013
A_52_P321342	Dock8	-1.253929978	0.460257271
A_52_P572476	Dhrs9	-1.251343166	0.460257271
A_51_P412200	Klf9	-1.249506191	0.460257271
A_51_P181705	5430405N12Rik	-1.243189903	0.460257271
A_52_P613087		-1.2351689	0.460257271
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A_52_P451644	Ndn	-1.230847666	0.460257271
A_52_P75777		-1.229477508	0.406336319
A_51_P503896	Pycr1	-1.228048718	0.440168683
A_51_P481261	Foxq1	-1.227943534	0.460257271
A_52_P112791	Mlstd2	-1.227918672	0.460257271
A_52_P548680		-1.227788205	0.460257271
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A_52_P635015	Gpr39	-1.225233312	0.458207734
A_52_P91823	B130024G19Rik	-1.225154169	0.460257271
A_52_P409076	Sema5a	-1.224338356	0.460257271
A_52_P313523	4930452B06Rik	-1.223859128	0.467401633
A_52_P525183	Acot2	-1.223049064	0.446702975
A_51_P336509	Zfpm2	-1.221722391	0.460257271
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A_51_P182471	Cugbp2	-1.215657223	0.460257271
A_51_P512525	Cfh	-1.214213349	0.460257271
A_51_P142153	4631422O05Rik	-1.214149124	0.460257271

A_51_P312348	Krt7	-1.213410071	0.473254072
A_51_P305532	Eif2s3x	-1.21313682	0.460257271
A_51_P314388	D530005L17Rik	-1.212275394	0.460257271
A_52_P367520	Nexn	-1.209368814	0.460257271
A_51_P449706	Lpp	-1.208516095	0.41562769
A_52_P415735	Zfp53	-1.207808436	0.460257271
A_51_P273157	Pde6h	-1.204513164	0.460257271
A_52_P523712	Tbx5	-1.203387835	0.561574461
A_51_P300806	Tlr4	-1.202227545	0.460257271
A_51_P372819	Ptgis	-1.198499276	0.626695325
A_51_P135802	Mef2c	-1.198463573	0.460257271
A_51_P500813	Lgals9	-1.196263845	0.460257271
A_51_P400659	Bcap29	-1.19218961	0.460257271
A_51_P504337	Entpd1	-1.19172124	0.438302037
A_51_P364485	Tnfaip2	-1.191402795	0.460257271
A_52_P574668	Nt5e	-1.190856625	0.473562325
A_51_P123765	Renbp	-1.19072903	0.460257271
A_51_P438967	Gpnmb	-1.189676565	0.460257271
A_52_P869091		-1.189520994	0.460257271
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A_51_P332917	Enpp3	-1.186280902	0.41562769
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A_52_P660693		-1.177431891	0.460257271
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A_51_P491350	Col4a2	-1.175557491	0.460257271
A_52_P215409	2810449C10Rik	-1.174986063	0.460257271
A_51_P149623	Gabrd	-1.172065397	0.460257271
A_51_P175581	Pcmtd1	-1.170580084	0.460257271
A_51_P210310		-1.169380956	0.460257271
A_52_P327764	Has2	-1.168267328	0.461162735

A_51_P500002	Sema6d	-1.166985428	0.461162735
A_51_P209327	Apln	-1.166757463	0.460257271
A_52_P159256	Lpp	-1.165607845	0.448390814
A_52_P512847	Jak3	-1.163896765	0.460257271
A_51_P415207	3110082D06Rik	-1.163696047	0.440750968
A_51_P431018	Selenbp2	-1.161708035	0.460257271
A_52_P518827	Col4a1	-1.160827219	0.460257271
A_51_P269216	Atf5	-1.1600317	0.404912554
A_52_P618745	D19Wsu12e	-1.159373034	0.404912554
A_51_P369224	Prdm8	-1.159322511	0.460257271
A_51_P284426	Cstad	-1.157348698	0.460257271
A_52_P511450	Mrpplf4	-1.156639079	0.475420437
A_52_P671769	Arhgap18	-1.154914988	0.460257271
A_52_P306351	Asph	-1.154408788	0.460257271
A_51_P473259	Dpyd	-1.152071787	0.460257271
A_51_P429308	Neto2	-1.146153225	0.460257271
A_51_P315344	A830058L05Rik	-1.143493752	0.460257271
A_52_P545810		-1.142937847	0.460257271
A_51_P159453	Serpi3n	-1.141825256	0.438302037
A_51_P456114	9930013L23Rik	-1.140254431	0.460257271
A_51_P404815	Apol6	-1.139898353	0.460257271
A_52_P494354	Mapk6	-1.138263886	0.460257271
A_52_P867663	Bicc1	-1.137668422	0.460257271
A_51_P499254	5830411E10Rik	-1.137487019	0.460257271
A_51_P463440	Elov16	-1.137466583	0.460257271
A_52_P361165	Ass1	-1.137427032	0.461162735
A_51_P105078	S100a4	-1.13549487	0.460257271
A_52_P175066	Cd2ap	-1.134770703	0.460257271
A_51_P162162	Inmt	-1.134611285	0.460257271
A_51_P305770	Emilin2	-1.133838887	0.460257271
A_51_P294535	Unc5b	-1.13320749	0.460257271

A_52_P638895	Vegfa	-1.131333088	0.460257271
A_52_P676819	Bnc1	-1.131074833	0.570237366
A_51_P503433	P pap2b	-1.130941673	0.460257271
A_52_P520859	Flt1	-1.130600964	0.460257271
A_52_P670812	0610007N19Rik	-1.129456363	0.460257271
A_52_P250400	Pcdh20	-1.12924157	0.460257271
A_52_P324934	Itga6	-1.128880699	0.460257271
A_52_P230938	Ly6c	-1.128379735	0.467401633
A_51_P496540	Sh2d1b1	-1.127439325	0.460257271
A_52_P1092823		-1.127300603	0.533567177
A_51_P437240	Emp2	-1.124654541	0.412853057
A_51_P377760	Rsel	-1.123936908	0.448390814
A_52_P223083	Pfkp	-1.122963158	0.460257271
A_51_P451458	Mamdc2	-1.121438158	0.460257271
A_51_P326152	Sim2	-1.121272368	0.460257271
A_51_P115005	Edn1	-1.120826403	0.558968282
A_51_P131315	Serpi9	-1.120337122	0.545337411
A_52_P646762	Smoc2	-1.1201448	0.460257271
A_51_P460048	1500041B16Rik	-1.120001065	0.460257271
A_51_P338713	Ass1	-1.119625023	0.461710604
A_51_P292127	Pgm2l1	-1.119138077	0.460257271
A_51_P401974	Enpp2	-1.118587165	0.515387348
A_51_P367434	Tmed5	-1.117865007	0.460257271
A_51_P406429	Pdk1	-1.117004821	0.460257271
A_51_P233059	Ktn1	-1.116541379	0.460257271
A_52_P448578	2600011C06Rik	-1.115214047	0.460257271
A_52_P33800	Fndc3a	-1.114051796	0.460257271
A_51_P295896	4930452B06Rik	-1.112943681	0.472686761
A_51_P355589	Fjx1	-1.112866166	0.460257271
A_51_P442366	Diap2	-1.11280869	0.460257271
A_52_P180728	Kbtbd11	-1.111689399	0.460257271

A_51_P487690	Ifi44	-1.11033185	0.460257271
A_51_P183400	Picalm	-1.108503419	0.460257271
A_52_P330694	Tle1	-1.108233751	0.458207734
A_51_P493886	Gpt2	-1.106010763	0.460257271
A_51_P296608	Gadd45a	-1.105879465	0.460257271
A_51_P306710	Cldn15	-1.104782728	0.604580299
A_51_P358722	Lancl3	-1.099926472	0.460257271
A_51_P287418	Man1a	-1.098287133	0.460257271
A_51_P259975	Aspa	-1.097541599	0.460257271
A_51_P368743	C630043F03Rik	-1.097133306	0.460257271
A_51_P146633	Bicc1	-1.097001499	0.460257271
A_51_P482585	1700049E17Rik	-1.096828542	0.460257271
A_51_P145541	Rbms1	-1.095948393	0.460257271
A_51_P216550	Trp63	-1.095309027	0.448390814
A_52_P620472	A830082K12Rik	-1.094663522	0.460257271
A_51_P103819	Trib2	-1.094298203	0.460257271
A_52_P458169	Adm2	-1.093845127	0.456133767
A_52_P113672	E030003F13Rik	-1.093090456	0.460257271
A_52_P172405		-1.092539708	0.460257271
A_51_P374752	Rbp4	-1.092440086	0.460257271
A_51_P356493	Bicc1	-1.087045709	0.461162735
A_52_P474266	Mfap3l	-1.084335314	0.460257271
A_51_P511060	Galct2	-1.084277853	0.460257271
A_51_P224872	Syne2	-1.083353184	0.460257271
A_52_P283055		-1.082673334	0.458207734
A_51_P468658	Aldh1l2	-1.081787673	0.460257271
A_51_P508402	Mical2	-1.081089859	0.460257271
A_52_P226559		-1.07978757	0.721534593
A_52_P564544	Fabp4	-1.079269325	0.460257271
A_51_P115441	Dpysl3	-1.078576745	0.461162735
A_51_P148612	Cox7a1	-1.077881293	0.481646787

A_52_P453650	1500011K16Rik	-1.07761178	0.460257271
A_52_P789489	Mtm1	-1.077150883	0.460257271
A_52_P496142	Col4a2	-1.076040649	0.460257271
A_52_P224348	Kctd12b	-1.073724919	0.460257271
A_52_P370268	Crisp1	-1.073722072	0.460257271
A_52_P629487	Selenbp1	-1.07286053	0.460257271
A_52_P631015	Etv5	-1.072857831	0.460257271
A_51_P464478		-1.072025939	0.460257271
A_51_P274259	Ak5	-1.070741331	0.441154035
A_52_P309022	Dach1	-1.069518473	0.486699561
A_51_P229886	Fpgt	-1.06908399	0.460257271
A_52_P843948	Foxg1	-1.068160623	0.460257271
A_51_P503352	D6Mm5e	-1.067541299	0.460257271
A_51_P407638	2900034E22Rik	-1.067493083	0.460257271
A_51_P161830	Enpep	-1.066484792	0.597328896
A_51_P104012	Tmem158	-1.065639643	0.460257271
A_51_P315931	Slco2a1	-1.064800185	0.460257271
A_52_P447534	D530005L17Rik	-1.062033883	0.460257271
A_51_P345626	Tnni3k	-1.06158535	0.460257271
A_51_P355629	Gas2	-1.06128322	0.440750968
A_51_P424878	2810405K02Rik	-1.059577485	0.483760388
A_51_P277884	Eif1a	-1.057963933	0.460257271
A_51_P155152	Ank	-1.057674413	0.460257271
A_52_P1026830	Tbc1d8b	-1.057401546	0.460257271
A_52_P603129	D230007K08Rik	-1.057317314	0.460257271
A_51_P151835		-1.056664895	0.460257271
A_51_P244531	6330403L08Rik	-1.056003355	0.460257271
A_52_P303161	Tuba8	-1.055944974	0.469535329
A_52_P526565	Pde1a	-1.055548703	0.555870788
A_51_P238659		-1.054904547	0.460257271
A_52_P421234	Rdh10	-1.053588844	0.498348138

A_52_P620399	Nr2f2	-1.052121887	0.460257271
A_51_P279100	Ptgs1	-1.051223959	0.5403658
A_51_P275016	Slc7a3	-1.050471777	0.54277937
A_51_P358423	Usp53	-1.049250617	0.460257271
A_51_P498322	Rasa1	-1.048992472	0.460257271
A_52_P62284	Apln	-1.04607148	0.486699561
A_51_P515605	Col3a1	-1.045907883	0.460257271
A_52_P144263	Rbms1	-1.045620486	0.460257271
A_52_P77793	Hs6st1	-1.044332193	0.460257271
A_51_P456113	9930013L23Rik	-1.043774772	0.461162735
A_51_P282523	Gpr124	-1.042274183	0.460257271
A_51_P308628		-1.042014642	0.460257271
A_52_P100909	Cugbp2	-1.042005071	0.460257271
A_51_P233534	Adamts5	-1.041545256	0.470684368
A_51_P480202	Dlx2	-1.041230644	0.533567177
A_51_P206849	2210418O10Rik	-1.040827757	0.460257271
A_52_P337126	Bves	-1.040761135	0.528512086
A_52_P432969	Pcdh19	-1.036922943	0.473254072
A_51_P245796	Ddit4	-1.036265822	0.481646787
A_52_P191412	Negr1	-1.036186786	0.460257271
A_51_P265327	Mpp6	-1.035516384	0.460257271
A_51_P327016	Pde1a	-1.033718914	0.581222692
A_51_P359636	Lgals3bp	-1.033292635	0.460257271
A_51_P187346	5133401H06Rik	-1.032726858	0.461162735
A_51_P269084	Ndg2	-1.032470866	0.460257271
A_51_P438479	Zfp281	-1.032328511	0.460257271
A_51_P161257	LOC627626	-1.031009999	0.441154035
A_51_P279389	Fut8	-1.030101073	0.460257271
A_52_P1083441	Ddx3y	-1.029410338	0.460257271
A_52_P429876	Tbx20	-1.029027106	0.460257271
A_52_P281702	Igfbp5	-1.027378684	0.461710604

A_52_P260856	Lpp	-1.026594574	0.460257271
A_51_P446192	2610101J03Rik	-1.026368548	0.460257271
A_52_P148212	C79407	-1.02260557	0.460257271
A_52_P186033	Spn	-1.022058696	0.467401633
A_52_P371494		-1.021562357	0.460257271
A_52_P660745	Sbf2	-1.020331088	0.460257271
A_51_P209150	Pcdh10	-1.018759117	0.460257271
A_51_P279323	Fkbp3	-1.018339317	0.460257271
A_52_P307739	Sox2	-1.018068722	0.590202834
A_52_P164136	Arrdc3	-1.016313774	0.460257271
A_52_P578268	Sec63	-1.01561291	0.460257271
A_51_P210143		-1.014400487	0.460257271
A_51_P140237	Fhl2	-1.013677263	0.460257271
A_52_P46102	Pde1a	-1.012671074	0.56437161
A_51_P350332	Rbpms	-1.012112838	0.460257271
A_52_P550147	Sned1	-1.010822931	0.460257271
A_52_P245119	Slc16a1	-1.010424998	0.460257271
A_52_P668900	Diap2	-1.010276063	0.460257271
A_52_P189038	Rbms1	-1.009923821	0.460257271
A_52_P100028	Rbpsuh	-1.008799775	0.4723445
A_51_P244287	Lamb1-1	-1.008774855	0.460257271
A_51_P324640	C330018D20Rik	-1.00860263	0.460257271
A_52_P527106		-1.008595849	0.460257271
A_51_P317141	Col2a1	-1.008450221	0.482733105
A_51_P193743	D230007K08Rik	-1.007923402	0.460257271
A_52_P249283	LOC385234	-1.007534065	0.470198489
A_51_P282616	4932425I24Rik	-1.007221867	0.460257271
A_51_P157154	Grin2d	-1.006197431	0.601395017
A_51_P209372	Sc4mol	-1.006039867	0.460257271
A_52_P577662	Ednrb	-1.005847281	0.455738846
A_52_P276748	Daam1	-1.003265984	0.460257271

A_51_P314077	Zfp53	-1.002368504	0.460257271
A_51_P436491	BC072620	-1.002322433	0.471468476
A_52_P307922	Flt1	-1.001822231	0.460257271
A_51_P228883	Htatip2	-1.00115971	0.486699561
A_51_P311476	Rgma	-1.000792937	0.460257271

Supplementary Table 5. Functional analysis of Gene Ontology terms for >2-fold downregulated genes in *Rap1*-null MEFs compared to wild-type MEFs. We found 104 overrepresented GO terms statistically significant (FDR<0.05) at Biological Process, Cellular Component and Molecular Function level. FDR=False Discovery Rate.

GO Term	FDR value
GO biological process at level 3	
multicellular organismal development (GO:0007275)	2.28E-16
anatomical structure development (GO:0048856)	3.50E-11
cell adhesion (GO:0007155)	4.24E-07
cellular developmental process (GO:0048869)	1.31E-06
localization of cell (GO:0051674)	3.26E-06
response to external stimulus (GO:0009605)	7.32E-06
defense response (GO:0006952)	2.13E-05
response to stress (GO:0006950)	7.34E-05
circulation (GO:0008015)	0.000619467
cell recognition (GO:0008037)	0.00547075
death (GO:0016265)	0.00802246
regulation of biological process (GO:0050789)	0.00802246
cell proliferation (GO:0008283)	0.00807251
tissue remodeling (GO:0048771)	0.00807251
behavior (GO:0007610)	0.0106598
regulation of a molecular function (GO:0065009)	0.0179208
reproductive process (GO:0022414)	0.0233572
excretion (GO:0007588)	0.0464939
GO biological process at level 4	
system development (GO:0048731)	6.59E-12
anatomical structure morphogenesis (GO:0009653)	6.39E-09
positive regulation of biological process (GO:0048518)	1.32E-07
cell differentiation (GO:0030154)	1.07E-06
cell motility (GO:0006928)	5.67E-06
response to wounding (GO:0009611)	0.000106511
embryonic development (GO:0009790)	0.000126304

pattern specification process (GO:0007389)	0.000640645
tube development (GO:0035295)	0.000640645
neuron recognition (GO:0008038)	0.000960628
regulation of developmental process (GO:0050793)	0.00126338
response to hypoxia (GO:0001666)	0.00634907
cell-substrate adhesion (GO:0031589)	0.0105643
blood pressure regulation (GO:0008217)	0.0105682
negative regulation of biological process (GO:0048519)	0.0105682
bone remodeling (GO:0046849)	0.0118593
hormone metabolic process (GO:0042445)	0.0149659
regulation of catalytic activity (GO:0050790)	0.0199492
cell-cell signaling (GO:0007267)	0.0331566
cell-cell adhesion (GO:0016337)	0.0331566
extracellular structure organization and biogenesis (GO:0043062)	0.0331566
regulation of cellular process (GO:0050794)	0.0331566
regulation of multicellular organismal process (GO:0051239)	0.0331566
fear response (GO:0042596)	0.0416927

GO biological process at level 5

organ development (GO:0048513)	5.31E-09
cell migration (GO:0016477)	4.34E-06
positive regulation of cellular process (GO:0048522)	3.06E-05
positive regulation of metabolic process (GO:0009893)	0.000149142
morphogenesis of a branching structure (GO:0001763)	0.000548935
nervous system development (GO:0007399)	0.000548935
inflammatory response (GO:0006954)	0.0018653
anatomical structure formation (GO:0048646)	0.0018653
cell morphogenesis (GO:0000902)	0.00273048
tube morphogenesis (GO:0035239)	0.00280291
negative regulation of enzyme activity (GO:0043086)	0.00306048
embryonic pattern specification (GO:0009880)	0.0039546

cell development (GO:0048468)	0.0039546
mesenchymal cell differentiation (GO:0048762)	0.00449603
regulation of cell differentiation (GO:0045595)	0.00465711
embryonic morphogenesis (GO:0048598)	0.00465711
regulation of transferase activity (GO:0051338)	0.0096162
cell-matrix adhesion (GO:0007160)	0.0125276
regionalization (GO:0003002)	0.0135963
extracellular matrix organization and biogenesis (GO:0030198)	0.0172523
cell fate commitment (GO:0045165)	0.0233846
positive regulation of developmental process (GO:0051094)	0.0312606

GO biological process at level 6

organ morphogenesis (GO:0009887)	1.32E-07
positive regulation of cellular metabolic process (GO:0031325)	0.000987056
branching morphogenesis of a tube (GO:0048754)	0.000987056
vasculature development (GO:0001944)	0.00111663
cellular morphogenesis during differentiation (GO:0000904)	0.00561763
skeletal development (GO:0001501)	0.00561763
enzyme linked receptor protein signaling pathway (GO:0007167)	0.00561763
sensory organ development (GO:0007423)	0.00561763
neurogenesis (GO:0022008)	0.00561763
mesenchymal cell development (GO:0014031)	0.00773258
cell projection morphogenesis (GO:0048858)	0.00945895
regulation of kinase activity (GO:0043549)	0.0146936
negative regulation of transferase activity (GO:0051348)	0.0212223
tissue development (GO:0009888)	0.0223951
cell death (GO:0008219)	0.0394404

GO biological process at level 7

blood vessel development (GO:0001568)	0.0248906
positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process (GO:0045935)	0.0305133

GO biological process at level 8

blood vessel morphogenesis (GO:0048514)	0.0294158
positive regulation of transcription (GO:0045941)	0.0466752
reproductive process in a multicellular organism (GO:0048609)	0.049652

GO cellular component at level 3

extracellular region part (GO:0044421)	9.24E-15
extracellular matrix part (GO:0044420)	0.0325022

GO cellular component at level 4

extracellular space (GO:0005615)	1.62E-13
proteinaceous extracellular matrix (GO:0005578)	5.50E-06

GO cellular component at level 5

plasma membrane (GO:0005886)	0.00359278
collagen (GO:0005581)	0.0259521
soluble fraction (GO:0005625)	0.0331493

GO cellular component at level 7

intrinsic to plasma membrane (GO:0031226)	0.000439368
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GO cellular component at level 8

integral to plasma membrane (GO:0005887)	0.00105389
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GO cellular component at level 9

intrinsic to organelle membrane (GO:0031300)	0.00813139
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GO molecular function at level 3

protein binding (GO:0005515)	0.0037672
pattern binding (GO:0001871)	0.0169058
extracellular matrix structural constituent (GO:0005201)	0.0466696
carbohydrate binding (GO:0030246)	0.0466696

GO molecular function at level 4

receptor binding (GO:0005102)	0.000480902
growth factor binding (GO:0019838)	0.0332513
extracellular matrix structural constituent conferring tensile strength (GO:0030020)	0.0332513

GO molecular function at level 5

growth factor activity (GO:0008083)	0.0043141
integrin binding (GO:0005178)	0.0411221
hormone activity (GO:0005179)	0.0481409

Supplementary Table 6. Functional analysis of Gene Ontology terms for >2-fold upregulated genes in *Rap1*-null MEFs compared to wild-type MEFs. The table shows those statistically significant overrepresented GO terms (FDR<0.05) at Biological Process, Cellular Component and Molecular Function level. FDR=False Discovery Rate.

GO Term	FDR value
GO biological process at level 3	
anatomical structure development (GO:0048856)	2.80E-09
multicellular organismal development (GO:0007275)	5.54E-07
cellular developmental process (GO:0048869)	0.00047983
localization of cell (GO:0051674)	0.00641526
establishment of localization (GO:0051234)	0.0077056
death (GO:0016265)	0.0137954
regulation of biological process (GO:0050789)	0.017062
nitrogen compound metabolic process (GO:0006807)	0.0284104
cell proliferation (GO:0008283)	0.0388613
GO biological process at level 4	
system development (GO:0048731)	3.44E-07
anatomical structure morphogenesis (GO:0009653)	5.94E-07
cell differentiation (GO:0030154)	0.00133012
cell motility (GO:0006928)	0.0185847
transport (GO:0006810)	0.0343974
GO cellular component at level 3	
extracellular region part (GO:0044421)	0.0299411
GO cellular component at level 4	
extracellular space (GO:0005615)	0.0381828
GO biological process at level 5	
organ development (GO:0048513)	2.43E-06
cell development (GO:0048468)	0.0316957
GO cellular component at level 9	
lytic vacuole (GO:0000323)	0.0428037
GO biological process at level 6	

organ morphogenesis (GO:0009887) **0.0205196**

GO molecular function at level 3

protein binding (GO:0005515) **0.00319946**

Supplementary Table 7. Genes involved in imprinting process were obtained from the Geneimprint database (URL: <http://www.geneimprint.com/site/genes-by-species.Mus+musculus>). Using Gene Set Enrichment Analysis this gene set was found significantly enriched in wild-type MEFs when compared to *Rap1*-deleted MEFs (FDR<0.001). The imprinting-related gene set components and their log fold-changes obtained from the microarray experiments are broken down below.

Gene Name	logFC KO/WT
MIRG	0.631049667
MEST	0.766245333
RIAN	0.575536
TFPI2	0.330578667
PEG10	0.231325
PPP1R9A	0.266780667
ASB4	0.549999333
NGFB	0.268645
CDKN1C	0.270541
GABRA5	0.104977
IGF2R	0.194788333
ZIM2	0.076146667
KCNQ1	0.065117
ASCL2	0.060641667
SDHD	0.131061667
OSBPL5	0.096276
CPA4	0.039392
COMM1D	0.088738333
SLC38A4	0.071588
PON1	0.035786
DLX5	0.024084667
INS1	0.011930667
TSSC4	0.016017333
SLC22A3	0.006210333

NAP1L5	-0.004367667
SLC22A2	-0.008233
GABRB3	-0.019822333
GNAS	-0.044865333
PON2	-0.039941
TNFRSF23	-0.027552667
CALCR	-0.035479667
L3MBTL	-0.050477333
TRPM5	-0.05761
ZIM1	-0.059902667
INS2	-0.076468333
TSIX	-0.073487333
NAP1L4	-0.231933667
XIST	-0.098547333
TRP73	-0.144258333
COPG2	-0.274241
IMPACT	-0.317002333
PON3	-0.332377
GRB10	-0.389614
SLC22A18	-0.242883667
GNAI3	-0.516401333
PEG12	-0.312634667
GATM	-0.277382
SGCE	-0.563088667
PLAGL1	-0.483630667
DDC	-0.26056
NNAT	-0.522234667
USP29	-0.272347
INPP5F	-0.485395
HTR2A	-0.293783667
CD81	-0.766005

DLK1	-0.938002667
UBE3A	-0.852535333
RASGRF1	-0.458118667
PHLDA2	-0.6796
ATP10A	-0.659234333
SNRPN	-0.859774667
PEG3	-0.937817333
NDN	-1.230848333
WT1	-2.060317333
DCN	-3.031471333
IGF2	-2.644036
H19	-3.569548

pSupplementary Table 8. Genes involved in cell adhesion were retrieved from KEGG database. Using Gene Set Enrichment Analysis, we found this gene set significantly upregulated in wild-type mice MEFs compared to *Rap1*-deleted MEFs (FDR=0.082). Cell Adhesion components and the corresponding log fold-changes are listed below.

CELL ADHESION	logFCKOvsWT
CD40	0.711733667
ITGB7	0.896441667
ICAM1	0.800964
MAG	0.623191667
CLDN7	0.438144
L1CAM	0.350468
CDH1	0.332311333
SDC3	0.521383333
4930412D23RIK	0.233135667
CD274	0.226811667
CLDN11	0.169253333
JAM3	0.342805
CD6	0.180592333
CD276	0.206343
NRXN2	0.208994667
ITGAL	0.149221667
NLGN1	0.126907
OCLN	0.119322
CDH2	0.183362667
CLDN5	0.118785
CD80	0.113791667
MADCAM1	0.112088333
CDH4	0.101493
CLDN14	0.103894667
NLGN3	0.079895667

VCAM1	0.143621667
NFASC	0.051370333
CD226	0.045933333
ICAM2	0.045611667
SDC4	0.090671
CTLA4	0.040888667
CLDN19	0.038620333
CD22	0.036178667
CLDN16	0.033356667
CD86	0.029683333
CD8B1	0.029219333
CLDN23	0.028908667
CLDN8	0.027800333
CNTN2	0.024228667
SELL	0.023306
CD28	0.023225667
CD8A	0.019760333
NRXN3	0.019041
PTPRC	0.017852
CD2	0.013194667
ITGAM	0.011039333
CLDN18	0.007983333
CLDN4	0.006768333
PDCD1	0.002765
ICOS	-0.003792667
PECAM1	-0.008603667
CDH5	-0.009075333
GLG1	-0.056582667
CLDN13	-0.023613333
CD40LG	-0.026671333
CLDN17	-0.028066667

NEO1	-0.064786
CLDN6	-0.032348333
ITGA4	-0.056930333
SELE	-0.058266
CD4	-0.062820667
MPZ	-0.066255333
CLDN2	-0.07624
PVRL1	-0.147170667
CNTNAP2	-0.080066333
CNTNAP1	-0.122232333
ITGB2L	-0.107814667
PDCD1LG2	-0.109212
NRXN1	-0.116861667
SDC1	-0.254581667
NCAM2	-0.126103667
F11R	-0.317336667
SDC2	-0.330428667
MPZL1	-0.350210333
CNTN1	-0.163037333
PVRL2	-0.323808
ITGB1	-0.399025
PTPRF	-0.492999667
ITGA9	-0.218143667
CLDN1	-0.255850667
CLDN9	-0.296126333
NCAM1	-0.536530667
GLYCAM1	-0.306047333
PVRL3	-0.599970333
ITGAV	-0.646454667
ITGB8	-0.481305
CD34	-0.937455667

CDH15	-0.466931
SELP	-0.493178
JAM2	-0.739178333
CDH3	-0.720376
PTPRM	-0.808663
CLDN15	-1.104782667
ITGB2	-0.723089667
4930468A15RIK	-0.681240333
SPN	-1.022058667
NEGR1	-1.036186333
CLDN3	-1.288548
ITGA6	-2.483593
ALCAM	-2.244807
ITGA8	-2.131300667

Supplementary Table 9. Genes involved in Regulation of Insulin Secretion pathway were retrieved from Reactome. We found that this gene set was found significantly enriched in wild-type MEFs compared to *Rap1*-null MEFs (FDR=0.106) applying Gene Set Enrichment Analysis to the IQR filtered dataset. Regulation of Insulin Secretion pathway components available in the microarray and their corresponding log fold-changes are listed below.

Regulation of Insulin Secretion Pathway Gene Set Log FC KOvsWT

	FABP4	-2.611377667
	PLA2G4A	-1.678464
	ADCY8	-1.615653667
	MGLL	-1.47694
	GDA	-1.435527667
	PYCR1	-1.228049
	DPYD	-1.152071667
	PPAP2B	-1.130941333
	GBE1	-0.811740667
	PCK2	-0.799536667
	CAV1	-0.767021667
	SUCLG2	-0.674752333
	CPOX	-0.666318333
	IQGAP1	-0.646418
	DLD	-0.524445333
	ADSS	-0.496624667
	SUCLA2	-0.488215333
	RPE	-0.485642
	CALM1	-0.479893667
	TKT	-0.387832667
	PGK1	-0.282482667
	ETFA	-0.247860667
	NDUFS1	-0.242307333
	CAMK4	-0.217796333
	COX7B	-0.145941333
	PKM2	-0.108005333

AMPD3	-0.088932333
ATP5F1	0.019205333
CYCS	0.051509667
ASL	0.090336
MARCKS	0.108218
NDUFA4	0.138698
SDHB	0.148253
PFKFB2	0.150942333
NDUFA5	0.198454667
NT5C2	0.234914333
NDUFB8	0.354319333
NDUFB2	0.362828667
AGPAT1	0.408178
NDUFB9	0.473113
VAMP2	0.497566333
NME1	0.562351333
SLC25A10	0.587565667
NDUFA11	0.611586
ARG1	0.846386
AMPD1	0.990345
AK1	1.017943
UPB1	1.342471

Supplementary Table 10. Genes involved in PPAR signalling pathway were retrieved from KEGG database. We found this pathway significantly upregulated in wild-type MEFs compared to Rap1-null MEFs (FDR=0.094) by Gene Set Enrichment Analysis. PPAR signalling pathway components and their corresponding log fold-changes are listed below.

PPAR SIGNALING PATHWAY	logFCKOvsWT
NR1H3	1.162985667
PPARA	0.95419
SLC27A4	0.890857333
SORBS1	0.853713
FABP7	0.468408
EHHADH	0.475456667
RXRA	0.446621667
SLC27A1	0.254218333
ACSL1	0.039275333
SCD1	-0.216656667
PCK2	-0.799536667
ACSL4	-1.290868333
PPARG	-1.330337333
ANGPTL4	-1.860048
FABP4	-2.611377667
UCP1	-2.977020667
LPL	-3.379085

Supplementary Table 11. Genes involved in Growth-hormone pathway were retrieved from Ingenuity IPA software. Using Gene Set Enrichment Analysis this gene set was found significantly enriched in wild-type MEFs compared to *Rap1*-null MEFs (FDR<0.006). Growth hormone pathway components and their log fold-changes observed in the microarray experiments are listed below.

Growth hormone Pathway Gene Set	logFC KO/WT
IGF1	0.220965667
GH	0.130591333
IRS1	0.374837667
SRF	0.348588333
STAT3	0.318923667
A2M	-0.012739667
JAK2	-0.218065333
STAT1	-0.360009333
GHR	-1.119357
PDK1	-1.117005333
IGFBP3	-2.022521667
IGF2	-2.644036
CEBPA	-0.560817767

Supplementary Table 12. Genes involved in Type II Diabetes Mellitus Pathway were collected from KEGG. This gene set was found significantly enriched in *Rap1*-deleted MEFs compared to wild-type MEFs (FDR<0.067) applying Gene Set Enrichment Analysis to IQR filtered dataset. Type II Diabetes Mellitus Pathway gene members and their log fold-changes are listed below.

Type II Diabetes Mellitus Pathway Gene Set	logFC KO/WT
SLC2A4	1.761263
PIK3R3	1.548617
ABCC8	0.956773
PIK3R5	1.049025333
CACNA1G	1.232758
PRKCZ	0.889768667
FRAP1	0.070407
IRS1	0.374837667
CACNA1B	0.127856333
PKM2	-0.108005333
PIK3R1	-0.107831333
MAPK1	-0.118614
SOCS4	-0.41865
PIK3CA	-0.555287333
CACNA1C	-0.773871667

Supplementary Table 13. Aging-related genes regulated by Caloric Restriction were obtained from Step et al, 2009. Using Gene Set Enrichment Analysis this gene set was found significantly enriched in wild-type MEFs compared to *Rap1*-null MEFs (FDR<0.02). Caloric restriction components used for enrichment analysis and their log fold-changes observed in the microarray experiments are listed below.

Gene Symbol	Log FC KO/WT
PPARA	0.95419
TERT	0.755443
NFKBIA	1.137571333
IGFALS	0.282329
GCLC	0.445335333
CAT	0.335137333
GCLM	0.27425
HSPA8	0.463125333
ARHGAP1	0.275687667
MAPK9	0.255754
STAT3	0.318923667
ERCC3	0.267687
VCP	0.293988667
SNCG	0.123381333
FOXO1	0.186798667
PDPK1	0.169282667
APTX	0.149408
PLAU	0.069726
GSTA4	0.052828333
TFDP1	0.071583
APEX1	0.062518667
LEPR	0.022911667
TXN1	-0.025342333
LMNB1	-0.126159333
PIK3R1	-0.107831333

JAK2	-0.218065333
MAPK3	-0.273839333
TOP2A	-0.301752333
CEPB	-0.373393333
EGFR	-0.31938
CDKN1A	-0.288842333
XRCC5	-0.399680667
CTSL	-0.604472667
MAP3K5	-0.391460333
NR3C1	-0.348058
BLM	-0.673734333
AR	-0.401683333
DDIT4	-1.036266
CEBPA	-0.560817333
PPARGC1A	-0.683622
JUN	-0.944628333
GHR	-1.119357
CEBD	-2.325273667
CTGF	-2.81585
FLT1	-1.894707667
NNMT	-3.961261333

Supplementary Table 14. ChIP-seq experiment summary. Overall reads and length obtained in Illumina ChIP-seq experiments. Two biological replicates per genotype (KO and WT) were processed, along a pool from all four input samples. Alignments on the NCBI37 genome assembly were made with Illumina's Eland software (GAPipeline 1.4.0), allowing for no more than 2 mismatches within 32 base seed lengths. % Align (PF), percentage of filtered reads that were uniquely aligned to the reference genome.

Sample ID	Raw Sequenced Reads	Size of Raw Sequenced Reads (bp)	% Align (PF)	Uniquely Mapped Reads	Size of Uniquely Mapped Reads (bp)
Rap1-wt2	19,757,812	711,281,232	55.3%	10,931,122	393,520,392
Rap1-ko1	21,564,675	776,328,300	49.2%	10,605,503	381,798,108
Rap1-ko2	15,015,951	540,574,236	48.2%	7,244,765	260,811,540
Rap1-wt1	19,094,194	687,390,984	55.0%	10,492,588	377,733,168
Pool of input samples	21,415,916	770,972,976	61.7%	13,203,284	475,318,224
Totals					
RAP1 ^{+/+} (WT)	38,852,006	1,398,672,216	55.1%	21,423,710	771,253,560
RAP1 ^{ΔΔ} (KO)	36,580,626	1,316,902,536	48.7%	17,850,268	642,609,648
Input	21,415,916	770,972,976	61.7%	13,203,284	475,318,224

Supplementary Table 15. *Rap1^{+/+}* raw sequencing reads are enriched in telomeric repeats. **a.** A significant ($p < 1.0E-26$) proportion (3.3368%) of the reads passing the quality control in the *Rap1^{+/+}* samples contain perfect occurrences of (TTAGGG)₅ or (CCCTAA)₅, as compared to the proportions in the Input DNA (0.0182% of the reads) or the *Rap1^{ΔΔ}* sample (0.0626% of the reads). The differences between the *Rap1^{ΔΔ}* sample and the Input pool are also significant, but this may well be due to the very large sample sizes. **b.** The telomeric repeat enrichment in the WT sample is specific, as the number of reads are even lower when examining another (less common in mouse genome) repeat, the satellite (ATTCC)₆, which appears in negligible proportions (<0.01%) of the reads across all samples. **c.** Detailed occurrences of telomeric and non-telomeric repeats in the raw reads sequenced across all the sequenced samples, displaying the inter-sample variability, but highlighting the enrichment of telomeric repeats in the *Rap1^{+/+}* sample.

	Total Raw QC Reads	Reads containing Repeat	(%)	Fold Input	
<i>Rap1^{+/+}</i>	32,920,359	1,098,499	3.3368%	182.92	
<i>Rap1^{ΔΔ}</i>	31,095,076	19,451	0.0626%	3.43	
Input	17,398,989	3,174	0.0182%	1.00	
a. Reads containing (TTAGGG) ₅ or (CCCTAA) ₅ in filtered output (s_n_sequence) Raw reads passing quality filtering, before alignment					
	Total Raw QC Reads	Reads containing Repeat	(%)	Fold Input	
<i>Rap1^{+/+}</i>	32,920,359	805	0.0024%	32.73	
<i>Rap1^{ΔΔ}</i>	31,095,076	1,639	0.0053%	70.55	
Input	17,398,989	13	<0.0001%	1.00	
b. Reads containing (ATTCC) ₆ or (GGAAT) ₆ in filtered output (s_n_sequence) Raw reads passing quality filtering, before alignment					
Repeat	Sample	Total Raw QC Reads	Reads containing Repeat	(%)	Fold Input
Telomeric					
(TTAGGG) ₅	<i>Rap1^{+/+}</i>	32,920,359	598,213	1.8172%	168.89
	wt1	16,406,927	373,238	2.2749%	211.43
	wt2	16,513,432	224,975	1.3624%	126.62
<i>Rap1^{ΔΔ}</i>	<i>Rap1^{ΔΔ}</i>	31,095,076	10,440	0.0336%	3.12
	ko1	17,783,406	5,913	0.0333%	3.09
	ko2	13,311,670	4,527	0.0340%	3.16
Input	Input	17,398,989	1,872	0.0108%	1.00
	<i>Rap1^{+/+}</i>	32,920,359	500,286	1.5197%	203.08
	wt1	16,406,927	324,576	1.9783%	264.36
(CCCTAA) ₅	wt2	16,513,432	175,710	1.0640%	142.19

	<i>Rap1</i>^{ΔΔ}	31,095,076	9,011	0.0290%	3.87
	ko1	17,783,406	4,824	0.0271%	3.62
	ko2	13,311,670	4,187	0.0315%	4.20
	Input	17,398,989	1,302	0.0075%	1.00
Non-telomeric					
(ATTCC)₆	<i>Rap1</i>^{+/+}	32,920,359	365	0.0011%	24.11
	wt1	16,406,927	225	0.0014%	29.83
	wt2	16,513,432	140	0.0008%	18.44
	<i>Rap1</i>^{ΔΔ}	31,095,076	770	0.0025%	53.86
(GGAAT)₆	ko1	17,783,406	367	0.0021%	44.88
	ko2	13,311,670	403	0.0030%	65.84
	Input	17,398,989	8	< 0.0001%	1.00
	<i>Rap1</i>^{+/+}	32,920,359	440	0.0013%	46.51
	wt1	16,406,927	259	0.0016%	54.93
	wt2	16,513,432	181	0.0011%	38.14
	<i>Rap1</i>^{ΔΔ}	31,095,076	869	0.0028%	97.25
	ko1	17,783,406	427	0.0024%	83.55
	ko2	13,311,670	442	0.0033%	115.54
	Input	17,398,989	5	< 0.0001%	1.00

c. In filtered output (s_n_sequence) – Raw reads passing quality filtering, before alignment

Supplementary Table 16. *In vivo* RAP1 binding peaks associated to differentially expressed genes (merged $|\log FC(WTvsKO)| \geq 1$)

Best ChIP-seq	Peak Rank	Mouse Chromosome	Peak Start Coordinate	Peak End Coordinate	Gene Name	RefSeq	logFC	Fold Change WTvsKO	Total Peaks in the Gene
	8,041	chr2	153,058,455	153,058,519	Tspyl3	NM_198617	-2.85	0.14	1
	3,909	chr15	102,810,727	102,810,787	Hoxc9	NM_008272	-2.20	0.22	1
	19,942	chr9	122,829,024	122,829,261	Zfp105	NM_009544	-1.88	0.27	1
	16,435	chr13	93,572,967	93,573,003	Thbs4	NM_011582	-1.84	0.28	2
	8,310	chr18	61,075,543	61,075,603	Arsi	NM_001038499	-1.81	0.28	1
	28,855	chr5	92,798,790	92,798,905	Cxcl11	NM_019494	-1.80	0.29	1
	15,247	chr11	70,024,064	70,024,129	Slc16a11	NM_153081	-1.72	0.30	1
	21,547	chr11	120,595,032	120,595,074	Cbr2	NM_007621	-1.71	0.31	1
	7,759	chr15	11,836,362	11,836,391	Npr3	NM_001039181	-1.69	0.31	1
	1,351	chr5	115,117,765	115,117,961	Trpv4	NM_022017	-1.67	0.31	2
	5,248	chr6	72,182,863	72,182,909	Atoh8	NM_153778	-1.57	0.34	2
	16,619	chr10	75,236,319	75,236,391	Ddt	NM_010027	-1.49	0.36	1
	19,015	chr11	70,845,405	70,845,441	6330403K07Rik	NM_134022	-1.47	0.36	1
	13,531	chr15	101,857,613	101,857,661	Krt18	NM_010664	-1.40	0.38	1
	9,400	chr9	54,398,490	54,398,566	Cib2	NM_019686	-1.39	0.38	1
	12,975	chr15	98,006,439	98,006,468	Al836003	NM_177716	-1.38	0.38	1
	668	chr3	126,065,437	126,065,517	Arsj	NM_173451	-1.37	0.39	1
	13,375	chr4	134,951,669	134,951,734	A330049M08Rik	NM_145555	-1.36	0.39	1
	3,122	chr9	87,617,952	87,618,029	Tbx18	NM_023814	-1.35	0.39	1
	19,115	chr10	74,866,876	74,866,909	Upb1	NM_133995	-1.34	0.39	1
	8,084	chr2	119,069,641	119,069,724	Sprint1	NM_016907	-1.33	0.40	1
	2,948	chr3	107,756,325	107,756,557	Gstm6	NM_008184	-1.33	0.40	2

1,630	chr13	51,935,181	51,935,227	Gadd45g	NM_011817	-1.32	0.40	2
24,462	chr3	95,482,314	95,482,351	Adamtsl4	NM_144899	-1.31	0.40	1
21,330	chr15	7,757,949	7,757,999	Gdnf	NM_010275	-1.26	0.42	1
7,103	chr9	120,455,671	120,455,741	Entpd3	NM_178676	-1.25	0.42	2
29,369	chr11	115,225,238	115,225,325	C630004H02Rik	NM_175454	-1.24	0.42	1
21,136	chr17	34,266,533	34,266,590	H2-DMa	NM_010386	-1.23	0.43	1
5,941	chr1	137,817,181	137,817,209	Pkp1	NM_019645	-1.20	0.43	3
22,912	chr8	98,239,509	98,239,586	Setd6	NM_001035123	-1.19	0.44	1
23,924	chr11	62,383,492	62,383,521	Trpv2	NM_011706	-1.18	0.44	2
1,219	chr19	34,558,205	34,558,299	Ch25h	NM_009890	-1.18	0.44	1
9,125	chr6	147,218,467	147,218,511	Pthlh	NM_008970	-1.17	0.44	1
4,128	chr19	30,242,732	30,242,805	Gldc	NM_138595	-1.17	0.45	1
11,933	chr2	32,232,604	32,232,642	1110008P14Rik	NM_198001	-1.16	0.45	1
17,686	chr2	91,029,748	91,029,776	Nr1h3	NM_013839	-1.16	0.45	1
8,304	chr5	67,072,747	67,072,785	Uchl1	NM_011670	-1.15	0.45	1
24,424	chr11	98,310,787	98,310,817	Grb7	NM_010346	-1.15	0.45	1
7,319	chr17	45,694,471	45,694,516	Nfkbie	NM_008690	-1.13	0.46	2
10,710	chr15	100,513,647	100,513,676	Ela1	NM_033612	-1.13	0.46	1
9,184	chr5	115,676,466	115,676,514	Pop5	NM_026398	-1.13	0.46	3
25,398	chr6	39,331,728	39,331,790	Rab19	NM_011226	-1.10	0.47	1
7,047	chr5	36,740,826	36,740,900	Sorcs2	NM_030889	-1.10	0.47	1
8,020	chr2	165,329,033	165,329,102	Slc2a10	NM_130451	-1.10	0.47	1
21,896	chr6	34,423,068	34,423,126	Bpgm	NM_007563	-1.10	0.47	1
4	chr2	28,040,118	28,040,149	Olfm1	NM_001038614	-1.10	0.47	1
5,855	chr4	154,715,102	154,715,141	Prkcz	NM_001039079	-1.10	0.47	1
20,728	chr3	142,249,041	142,249,094	Gbp1	NM_010259	-1.07	0.48	1
2,853	chr6	72,331,695	72,331,736	Vamp5	NM_001080742	-1.07	0.48	1
19,128	chr10	43,305,102	43,305,174	Cd24a	NM_009846	-1.06	0.48	1

22,064	chr14	55,031,692	55,031,722	Slc7a7	NM_011405	-1.05	0.48	1
2,102	chr6	71,647,979	71,648,065	Reep1	NM_178608	-1.04	0.49	1
16,517	chr11	103,118,881	103,118,929	Map3k14	NM_016896	-1.03	0.49	1
8,586	chr2	154,228,856	154,228,884	Snta1	NM_009228	-1.02	0.49	1
24,970	chr16	22,433,674	22,433,971	Etv5	NM_023794	1.00	2.00	1
9,846	chr10	80,301,574	80,301,632	BC072620	NM_001013758	1.00	2.00	1
12,756	chr1	17,092,992	17,093,045	Jph1	NM_020604	1.01	2.02	1
7,650	chr13	81,028,719	81,028,985	Arrdc3	NM_001042591	1.02	2.02	1
18,383	chr3	34,555,369	34,555,429	Sox2	NM_011443	1.02	2.03	1
11,995	chr17	14,416,235	14,416,269	Smoc2	NM_022315	1.03	2.04	1
27,820	chr10	75,403,362	75,403,398	Ndg2	NM_175329	1.03	2.05	1
1,412	chr3	37,313,610	37,313,645	Nudt6	NM_153561	1.03	2.05	2
14,404	chr10	59,405,815	59,405,867	Ddit4	NM_029083	1.04	2.05	1
17,855	chrX	138,821,792	138,821,851	Acsl4	NM_001033600	1.04	2.06	1
22,659	chr2	71,380,282	71,380,506	Dlx2	NM_010054	1.04	2.06	1
11,001	chr8	28,199,849	28,199,925	Gpr124	NM_054044	1.04	2.06	1
23,451	chr2	36,087,127	36,087,163	Ptgs1	NM_008969	1.05	2.07	1
25,367	chr7	59,134,974	59,135,172	Gas2	NM_008087	1.06	2.09	1
30,069	chr6	4,457,414	4,457,442	Col1a2	NM_007743	1.07	2.09	1
16,966	chr6	82,898,439	82,898,469	D6Mm5e	NM_033079	1.07	2.10	1
1,752	chr2	65,961,960	65,962,041	Galnt3	NM_015736	1.07	2.10	2
23,858	chr12	82,736,801	82,736,844	Ttc9	NM_001033149	1.08	2.12	1
841	chr19	38,200,547	38,200,616	Rbp4	NM_011255	1.09	2.13	1
27,541	chr5	137,452,510	137,452,557	Cldn15	NM_021719	1.10	2.15	1
3,871	chr6	66,992,044	66,992,073	Gadd45a	NM_007836	1.11	2.15	2
2,583	chr8	88,010,051	88,010,135	Gpt2	NM_173866	1.11	2.15	1
8,321	chr9	92,178,383	92,178,428	Plscr2	NM_008880	1.12	2.17	1
16,777	chr5	108,561,205	108,561,268	Tmed5	NM_028876	1.12	2.17	1

12,091	chr12	105,255,173	105,255,242	Serpina9	NM_027997	1.12	2.17	1
4,425	chr1	155,404,248	155,404,356	Npl	NM_028749	1.13	2.18	2
6,057	chr14	88,874,009	88,874,084	Pcdh20	NM_178685	1.13	2.19	1
10,990	chr10	60,291,949	60,292,001	Unc5b	NM_029770	1.13	2.19	1
29,526	chr2	128,523,880	128,523,909	Mertk	NM_008587	1.15	2.22	1
4,802	chr10	119,911,009	119,911,074	Hmga2	NM_010441	1.15	2.22	3
2,539	chr2	30,454,935	30,454,978	Cstad	NM_030137	1.16	2.23	1
3,068	chr10	13,589,597	13,589,626	Aig1	NM_025446	1.18	2.26	2
15,282	chr12	112,675,726	112,675,782	Tnfaip2	NM_009396	1.19	2.28	1
8,288	chr17	71,661,289	71,661,352	Emilin2	NM_145158	1.20	2.29	3
21,591	chr11	78,788,945	78,789,022	Lgals9	NM_010708	1.20	2.29	1
17,491	chr2	167,056,578	167,056,636	Ptgis	NM_008968	1.20	2.30	2
4,159	chrX	153,854,314	153,854,358	Phex	NM_011077	1.22	2.33	1
4,649	chr12	85,332,555	85,332,644	Acot2	NM_134188	1.22	2.33	2
2,221	chr17	24,130,688	24,130,761	Prss22	NM_133731	1.23	2.34	1
30,259	chr11	120,510,867	120,511,151	Pycr1	NM_144795	1.23	2.34	1
15,404	chr12	15,817,214	15,817,275	Trib2	NM_144551	1.23	2.34	1
17,223	chr6	52,114,567	52,114,622	Hoxa2	NM_010451	1.23	2.35	1
8,438	chr6	135,118,358	135,118,400	Hebp1	NM_013546	1.23	2.35	2
176	chr16	22,900,460	22,900,520	Ahsg	NM_013465	1.25	2.38	1
24,934	chr5	135,452,083	135,452,225	Cldn3	NM_009902	1.29	2.44	1
18,938	chr12	75,004,374	75,004,421	Hif1a	NM_010431	1.29	2.45	1
8,512	chr7	146,092,995	146,093,042	Bnip3	NM_009760	1.30	2.46	1
4,330	chr17	74,298,496	74,298,525	Xdh	NM_011723	1.30	2.47	4
18,041	chr7	126,144,986	126,145,015	Gprc5b	NM_022420	1.31	2.48	1
18,105	chr6	115,371,964	115,372,017	Pparg	NM_011146	1.33	2.51	1
6,750	chr12	50,483,330	50,483,409	Foxg1	NM_008241	1.34	2.54	1
3,356	chr13	119,507,698	119,507,908	Fgf10	NM_008002	1.35	2.54	1

7,876	chr9	102,911,603	102,911,684	Slco2a1	NM_033314	1.36	2.56	3
2,921	chr2	122,530,554	122,530,593	Slc30a4	NM_011774	1.36	2.56	3
5,633	chr2	12,224,375	12,224,440	Itga8	NM_001001309	1.36	2.56	1
12,445	chrX	163,646,952	163,647,362	Tmsb4x	NM_021278	1.36	2.57	1
9,891	chr7	28,117,382	28,117,462	Ltbp4	NM_175641	1.38	2.60	1
11,039	chr16	52,449,080	52,449,139	Alcam	NM_009655	1.39	2.61	1
13,050	chr10	82,997,022	82,997,096	Aldh1l2	NM_153543	1.39	2.62	2
10,737	chr4	137,557,983	137,558,102	Eif4g3	NM_172703	1.40	2.64	1
24,159	chr7	111,615,608	111,615,638	Trim30	NM_009099	1.41	2.65	1
26,585	chr5	91,322,403	91,322,451	Cxcl1	NM_008176	1.43	2.70	1
707	chr13	16,114,008	16,114,120	Inhba	NM_008380	1.44	2.72	2
16,391	chr14	66,582,164	66,582,222	Clu	NM_013492	1.45	2.74	1
20,100	chr8	74,211,340	74,211,434	Insl3	NM_013564	1.46	2.74	1
12,906	chr1	151,944,568	151,944,640	Ptgs2	NM_011198	1.47	2.76	1
4,558	chr7	135,137,843	135,137,876	Pycard	NM_023258	1.49	2.81	1
11,744	chr8	47,076,739	47,076,767	Ankrd37	NM_001039562	1.50	2.83	2
28,778	chr2	148,234,909	148,235,112	Thbd	NM_009378	1.52	2.86	1
14,554	chr3	144,488,236	144,488,266	Clca2	NM_030601	1.52	2.87	1
7,161	chr3	79,689,612	79,689,672	1110032E23Rik	NM_133187	1.52	2.88	1
3,070	chr4	150,236,587	150,236,631	Errfi1	NM_133753	1.53	2.88	4
13,269	chr14	45,938,766	45,938,823	Ero1l	NM_015774	1.54	2.90	1
5,241	chr2	109,521,179	109,521,356	Bdnf	NM_001048139	1.55	2.93	2
561	chr1	40,496,711	40,496,796	Il1rl1	NM_010743	1.55	2.94	3
10,952	chr14	111,153,190	111,153,243	Slitrk6	NM_175499	1.57	2.97	2
8,570	chr3	80,833,525	80,833,580	Pdgfc	NM_019971	1.59	3.00	1
21,458	chr13	33,053,717	33,053,767	Serpinb6b	NM_011454	1.60	3.03	1
8,054	chr3	54,157,340	54,157,408	Postn	NM_015784	1.60	3.03	1
16,340	chr15	64,754,567	64,754,634	Adcy8	NM_009623	1.62	3.06	1

19,959	chr2	162,812,891	162,812,982	Sgk2	NM_013731	1.63	3.10	1
13,654	chr9	7,554,892	7,554,934	Mmp8	NM_008611	1.64	3.12	1
15,172	chrX	10,301,988	10,302,076	Mid1ip1	NM_026524	1.64	3.12	2
6,697	chr9	103,010,812	103,010,889	Rab6b	NM_173781	1.64	3.12	1
19,991	chr15	34,236,364	34,236,421	Matn2	NM_016762	1.66	3.17	1
4,634	chr15	56,523,898	56,523,970	Has2	NM_008216	1.66	3.17	2
9,017	chr7	149,667,200	149,667,333	Lsp1	NM_019391	1.67	3.18	1
21,371	chr14	59,975,839	59,975,875	D14Ert668e	NM_199015	1.67	3.19	1
3,544	chr13	115,250,995	115,251,048	Fst	NM_008046	1.69	3.23	2
28,993	chr7	142,729,050	142,729,280	Ptpre	NM_011212	1.70	3.25	1
17,524	chr6	136,817,559	136,817,605	Mgp	NM_008597	1.72	3.29	2
7,723	chr10	98,732,095	98,732,157	Dusp6	NM_026268	1.72	3.30	1
19,685	chr2	119,180,121	119,180,437	Chac1	NM_026929	1.73	3.31	1
23,122	chr5	75,552,763	75,552,804	Pdgfra	NM_001083316	1.74	3.34	1
3,721	chr3	57,098,644	57,098,733	Tm4sf1	NM_008536	1.76	3.38	3
10,421	chr15	67,006,214	67,006,243	St3gal1	NM_009177	1.81	3.51	1
1,770	chr7	152,117,835	152,117,892	Ccnd1	NM_007631	1.84	3.57	2
764	chr1	12,701,710	12,701,939	Sulf1	NM_172294	1.84	3.58	1
260	chr17	33,920,665	33,920,732	Angptl4	NM_020581	1.86	3.63	3
14,996	chr7	52,861,366	52,861,443	Fgf21	NM_020013	1.87	3.65	1
166	chr3	19,857,063	19,857,144	Cp	NM_007752	1.87	3.65	1
15,758	chr9	43,857,719	43,857,747	Thy1	NM_009382	1.93	3.81	2
7,931	chr18	70,075,858	70,075,931	Ccdc68	NM_201362	1.99	3.97	1
19,335	chr11	74,972,250	74,972,307	Hic1	NM_001098203	2.01	4.02	4
108	chr5	136,521,377	136,521,454	Upk3b	NM_175309	2.12	4.34	2
15,741	chr9	71,058,842	71,058,871	Aldh1a2	NM_009022	2.14	4.42	1
23,666	chr16	15,896,407	15,896,454	Cebpd	NM_007679	2.33	5.01	1
4,997	chr5	104,870,704	104,870,746	Spp1	NM_009263	2.34	5.07	1

6,644	chr6	55,289,363	55,289,459	Aqp1	NM_007472	2.35	5.11	1
726	chr1	51,347,795	51,347,861	Sdpr	NM_138741	2.38	5.20	2
7,315	chr5	98,687,631	98,687,670	Fgf5	NM_010203	2.39	5.24	2
8,218	chr11	28,766,736	28,766,797	Efemp1	NM_146015	2.39	5.25	1
4,338	chr13	113,993,859	113,993,950	Esm1	NM_023612	2.43	5.38	3
29,521	chr9	54,613,901	54,614,084	Crabp1	NM_013496	2.58	5.98	1
11,678	chrY	346,925	346,969	Eif2s3y	NM_012011	2.70	6.48	1
2,675	chr10	24,308,726	24,308,800	Ctgf	NM_010217	2.82	7.04	2
7,754	chr1	155,587,478	155,587,539	Rgs16	NM_011267	3.12	8.72	1
1,901	chr3	131,747,064	131,747,130	Dkk2	NM_020265	3.72	13.17	2
5,374	chr4	147,883,856	147,883,884	Angptl7	NM_001039554	3.75	13.48	1

Supplementary Table 17. *In vivo* RAP1 binding peaks associated to differentially expressed genes (merged $|\log FC(WTvsKO)| \geq 1$) with TTAGGG telomeric motifs (Perfect Motifs = PM; 1 Mismatch = MM) in the peak sequences. Out of the 173 deregulated genes that have associated binding peaks, 89 (51%) present at least one TTAGGG motif. LogFCs in green represent the 23 downregulated genes with telomeric motifs in their peak sequences, while LogFCs in red represent the 66 upregulated genes.

Peak									
Rank	Chromosome	Peak Start	Peak End	Gene	RefSeq	LogFC(WTvsKO)	Motifs in Peaks	PM Motifs	MM Motifs
8,041	chr2	153,058,455	153,058,519	Tspyl3	NM_198617	-2.84762	1	0	1
19,942	chr9	122,829,024	122,829,261	Zfp105	NM_009544	-1.87514	1	0	1
8,310	chr18	61,075,543	61,075,603	Arsi	NM_001038499	-1.81318	1	0	1
28,855	chr5	92,798,790	92,798,905	Cxcl11	NM_019494	-1.79951	2	0	2
21,547	chr11	120,595,032	120,595,074	Cbr2	NM_007621	-1.71077	2	0	2
1,351	chr5	115,117,765	115,117,961	Trpv4	NM_022017	-1.67026	1	0	1
5,248	chr6	72,182,863	72,182,909	Atoh8	NM_153778	-1.57191	1	0	1
9,400	chr9	54,398,490	54,398,566	Cib2	NM_019686	-1.39048	3	0	3
3,122	chr9	87,617,952	87,618,029	Tbx18	NM_023814	-1.34927	1	0	1
2,948	chr3	107,756,325	107,756,557	Gstm6	NM_008184	-1.33171	5	0	5
6,107	chr13	51,941,757	51,941,795	Gadd45g	NM_011817	-1.32491	1	0	1
29,369	chr11	115,225,238	115,225,325	C630004H02Rik	NM_175454	-1.23531	3	0	3
12,508	chr1	137,814,071	137,814,422	Pkp1	NM_019645	-1.20200	3	0	3
22,912	chr8	98,239,509	98,239,586	Setd6	NM_001035123	-1.18755	3	0	3
28,983	chr11	62,387,743	62,387,771	Trpv2	NM_011706	-1.18213	1	0	1
4,128	chr19	30,242,732	30,242,805	Gldc	NM_138595	-1.16741	2	0	2
7,319	chr17	45,694,471	45,694,516	Nfkbie	NM_008690	-1.13137	2	0	2
12,308	chr5	115,686,029	115,686,094	Pop5	NM_026398	-1.12878	2	0	2
8,020	chr2	165,329,033	165,329,102	Slc2a10	NM_130451	-1.09809	1	0	1
4	chr2	28,040,118	28,040,149	Olfm1	NM_001038614	-1.09582	5	3	2
2,102	chr6	71,647,979	71,648,065	Reep1	NM_178608	-1.03751	1	0	1
16,517	chr11	103,118,881	103,118,929	Map3k14	NM_016896	-1.02544	3	0	3
8,586	chr2	154,228,856	154,228,884	Snta1	NM_009228	-1.01882	1	0	1
24,970	chr16	22,433,674	22,433,971	Etv5	NM_023794	1.00026	4	0	4

9,846	chr10	80,301,574	80,301,632	BC072620	NM_001013758	1.00232	1	0	1
7,650	chr13	81,028,719	81,028,985	Arrdc3	NM_001042591	1.01631	2	0	2
18,383	chr3	34,555,369	34,555,429	Sox2	NM_011443	1.01807	2	0	2
11,995	chr17	14,416,235	14,416,269	Smoc2	NM_022315	1.03084	1	0	1
27,820	chr10	75,403,362	75,403,398	Ndg2	NM_175329	1.03247	1	0	1
22,659	chr2	71,380,282	71,380,506	Dlx2	NM_010054	1.04123	1	1	0
11,001	chr8	28,199,849	28,199,925	Gpr124	NM_054044	1.04227	2	0	2
25,367	chr7	59,134,974	59,135,172	Gas2	NM_008087	1.06128	2	0	2
30,069	chr6	4,457,414	4,457,442	Col1a2	NM_007743	1.06619	1	1	0
1,752	chr2	65,961,960	65,962,041	Galnt3	NM_015736	1.07244	1	0	1
27,541	chr5	137,452,510	137,452,557	Cldn15	NM_021719	1.10478	1	0	1
2,583	chr8	88,010,051	88,010,135	Gpt2	NM_173866	1.10601	1	0	1
8,321	chr9	92,178,383	92,178,428	Plscr2	NM_008880	1.11668	2	0	2
10,990	chr10	60,291,949	60,292,001	Unc5b	NM_029770	1.13321	2	0	2
19,078	chr10	119,906,850	119,906,911	Hmga2	NM_010441	1.15351	1	0	1
2,539	chr2	30,454,935	30,454,978	Cstad	NM_030137	1.15735	1	0	1
19,972	chr17	71,651,106	71,651,338	Emilin2	NM_145158	1.19508	3	0	3
21,591	chr11	78,788,945	78,789,022	Lgals9	NM_010708	1.19626	2	0	2
6,137	chr12	85,328,522	85,328,571	Acot2	NM_134188	1.22305	1	0	1
30,259	chr11	120,510,867	120,511,151	Pycr1	NM_144795	1.22805	1	0	1
176	chr16	22,900,460	22,900,520	Ahsg	NM_013465	1.25019	1	0	1
24,934	chr5	135,452,083	135,452,225	Cldn3	NM_009902	1.28855	2	0	2
18,938	chr12	75,004,374	75,004,421	Hif1a	NM_010431	1.29241	2	0	2
18,105	chr6	115,371,964	115,372,017	Pparg	NM_011146	1.33034	1	0	1
6,750	chr12	50,483,330	50,483,409	Foxg1	NM_008241	1.34307	2	0	2
3,356	chr13	119,507,698	119,507,908	Fgf10	NM_008002	1.34704	2	0	2
9,105	chr9	102,916,091	102,916,144	Slco2a1	NM_033314	1.35619	4	0	4
17,001	chr2	122,523,616	122,523,727	Slc30a4	NM_011774	1.35633	4	0	4
5,633	chr2	12,224,375	12,224,440	Itga8	NM_001001309	1.35889	2	0	2

12,445	chrX	163,646,952	163,647,362	Tmsb4x	NM_021278	1.36312	2	0	2
9,891	chr7	28,117,382	28,117,462	Ltbp4	NM_175641	1.38051	1	0	1
13,050	chr10	82,997,022	82,997,096	Aldh1l2	NM_153543	1.38845	2	0	2
10,737	chr4	137,557,983	137,558,102	Eif4g3	NM_172703	1.40242	2	0	2
26,585	chr5	91,322,403	91,322,451	Cxcl1	NM_008176	1.43370	1	0	1
4,348	chr13	16,110,326	16,110,443	Inhba	NM_008380	1.44295	1	0	1
12,906	chr1	151,944,568	151,944,640	Ptgs2	NM_011198	1.46597	2	0	2
29,030	chr8	47,081,752	47,081,781	Ankrd37	NM_001039562	1.49903	1	0	1
28,778	chr2	148,234,909	148,235,112	Thbd	NM_009378	1.51646	1	0	1
3,590	chr4	150,231,991	150,232,106	Errfi1	NM_133753	1.52729	4	0	4
13,269	chr14	45,938,766	45,938,823	Ero1l	NM_015774	1.53749	2	0	2
5,241	chr2	109,521,179	109,521,356	Bdnf	NM_001048139	1.55190	5	0	5
578	chr1	40,501,663	40,501,718	Il1rl1	NM_001025602	1.55369	6	0	6
30,328	chr14	111,149,150	111,149,292	Slitrk6	NM_175499	1.56832	1	0	1
16,340	chr15	64,754,567	64,754,634	Adcy8	NM_009623	1.61565	1	0	1
19,959	chr2	162,812,891	162,812,982	Sgk2	NM_013731	1.63450	1	0	1
15,172	chrX	10,301,988	10,302,076	Mid1ip1	NM_026524	1.64155	2	0	2
6,697	chr9	103,010,812	103,010,889	Rab6b	NM_173781	1.64250	1	0	1
8,312	chr15	56,518,622	56,518,662	Has2	NM_008216	1.66389	1	0	1
9,017	chr7	149,667,200	149,667,333	Lsp1	NM_019391	1.66737	1	0	1
3,544	chr13	115,250,995	115,251,048	Fst	NM_008046	1.69342	3	0	3
28,993	chr7	142,729,050	142,729,280	Ptpre	NM_011212	1.70055	1	0	1
19,685	chr2	119,180,121	119,180,437	Chac1	NM_026929	1.72827	6	0	6
28,808	chr3	57,097,044	57,097,119	Tm4sf1	NM_008536	1.75580	1	0	1
1,461	chr17	33,921,823	33,921,886	Angptl4	NM_020581	1.86005	4	0	4
166	chr3	19,857,063	19,857,144	Cp	NM_007752	1.86792	1	0	1
7,931	chr18	70,075,858	70,075,931	Ccdc68	NM_201362	1.98779	2	0	2
22,644	chr11	74,981,303	74,981,393	Hic1	NM_001098203	2.00820	2	0	2
108	chr5	136,521,377	136,521,454	Upk3b	NM_175309	2.11797	3	0	3

6,644	chr6	55,289,363	55,289,459	Aqp1	NM_007472	2.35313	1	1	0
726	chr1	51,347,795	51,347,861	Sdpr	NM_138741	2.37839	2	0	2
7,315	chr5	98,687,631	98,687,670	Fgf5	NM_010203	2.38847	1	0	1
4,338	chr13	113,993,859	113,993,950	Esm1	NM_023612	2.42682	2	0	2
29,521	chr9	54,613,901	54,614,084	Crabp1	NM_013496	2.57896	2	0	2
2,675	chr10	24,308,726	24,308,800	Ctgf	NM_010217	2.81585	2	0	2
1,901	chr3	131,747,064	131,747,130	Dkk2	NM_020265	3.71903	1	0	1

Supplementary Table 18. Weeder motifs found in Jaspar and Transfac for the top 10, 30, 50, 100 and 200 ranking peaks (excluding those with telomeric motifs).

Jaspar	Top10	Top30	Top50	Top100	Top200
SQUA	2.52E-04	3.37E-04			1.48E-02
HMG-IY	5.52E-04	9.07E-06	5.94E-05		
id1	1.08E-03	1.93E-05	1.55E-03		
dl_1	1.34E-03		6.51E-03	4.12E-03	
Pax4	6.26E-03			3.00E-02	
MEF2A	1.00E-02				
Foxd3	1.16E-02	6.50E-04	1.81E-04		
MNB1A	1.17E-02	7.43E-03			
FOXD1	1.52E-02			7.95E-03	
Klf4	1.54E-02				
Broad-complex_1		4.53E-04	2.48E-04		2.13E-02
IRF1		2.11E-03			
RUNX1		8.50E-03	8.66E-03	4.78E-03	3.27E-03
STAT1		1.03E-02			
hb		1.13E-02			
Broad-complex_4			8.64E-03		
Foxq1			9.72E-03		
FOXI1			1.85E-02		
T				6.65E-04	
RREB1				2.25E-03	
ZNF354C				5.73E-03	
En1				8.30E-03	
BRCA1				1.02E-02	
sna				3.00E-02	
Evi1					6.47E-04
ELK4					1.84E-03
Eip74EF					3.57E-03
GABPA					3.58E-03
ELK1					2.00E-02
TAL1-TCF3					2.07E-02
Hand1-Tcfe2a					3.33E-02

Transfac	Top10	Top30	Top50	Top100	Top200
BR-C	6.15E-06	3.49E-05	7.87E-05		
ID1	7.08E-06	1.92E-05			
FOXP1	6.87E-05	1.99E-06	3.53E-07	4.06E-05	
FACB	8.95E-05				
dl	1.09E-04				
MEF-2	2.10E-04				
MADS-B	2.78E-04	9.36E-06			

STE11	3.62E-04	3.30E-06	3.07E-06
MYB.Ph3	3.78E-04		
Grainyhead-Elf-1-NTF-1	5.45E-04		6.32E-06
AG	1.56E-07		
MADS-A	2.58E-05		
HFH4	1.71E-04	8.65E-06	
IRF-1	1.96E-04		
Antp	4.34E-05		
HSF	7.24E-05		8.73E-06
Hb	1.58E-04		
FOXD3	2.16E-04		
XFD-3	2.87E-04		
AML1	2.07E-05		
AML1a	3.03E-05		
FOXP3	5.29E-05		
Poly	6.81E-05	8.15E-05	
GBF	6.90E-04		
TBX5	7.15E-04		
ACAAT	9.55E-04		
AP-2rep	9.68E-04		
RREB-1	1.44E-03		
Rim101p	2.14E-05		
Evi-1	6.92E-05		
dTCF	7.50E-05		
PEBP	8.57E-05		
Osf2	1.74E-04		

Table S19.

Name	Sequence 5'-3'
Primers used for confirmation of <i>Rap1-exon3</i> excision	
24C10-F	TCTGCAGCCCACATTCCATA
26C2-R	CTGTAAATGACCTCACGGACCA
Primers used for real time qPCR	
RAP1-1F	AAGGACCGCTACCTTAAGCA
RAP1-1R	TGTTGTCTGCCTCTCCATTC
RAP1-2F	CTTGGTCCACTTGCTGTGT
RAP1-2R	TGAGACACATCCTCCCTCA
KARS-F	GAAGCTGCCAGAAACCAGTC
KARS-R	TGCATGTGACTTCGAGGAAC
HS3ST1-F	AGCCTGTACCATGCACACAT
HS3ST1-R	CCTTGGAACCTGTGAAAGCA
NNMT-F	ATGGAATCTGGCTTCACCTC
NNMT-R	CAGGCAGAGAGAAGCTGATAGA
CAR6-F	CCTGAGCTTGGTGAACATATGAG
CAR6-R	GTGAACAAAGTGAGCCTCCA
IGF2-F	GCTTGTGACACGCTTCAGT
IGF2-R	TGAGCTCTTGGCAAGCA
H19-F	AGGATGACAGGTGTGGTCAA
H19-R	TGAGTGAGTGGGTGGACAAT
CTGF-F	CTCTGCCAGTGGAGTTCAAA
CTGF-R	TACGCCATGTCTCCGTACAT
SLIT3-F	AGAGGGCATCGTGGAAATAC
SLIT3-R	AGCGACGTGAGTGAGTTCA
GRIA3-F	GCAGAGAAAGCCGTGTGATA
GRIA3-R	CCACATTGCTCAGGCTTAGA
STMN2-F	ATCTTGAAAGCCACCATCTCC
STMN2-R	CTTCTCTGCCAACTGCTTCA
ADRA2-F	GAATCATGGCTGTGGAGATG
ADRA2-R	GCAGAGGCTTCATTCCTTC
EPB4.1I4a-F	CCAGGAGAATGACATGGTG
EPB4.1I4a-R	AGCTCCTCTGGATGTGCTT
NUDT6-F	AATTCAAGGCCCTGTTGAGC
NUDT6-R	TTCCCTGAGTCCATACAGCA
IFI27-F	TGTTTGGCTCTGCCATAGG
IFI27-R	TTGATGTGGAGAGTCCAAGG
ENED-F	TGAGTGAAAGTGTTCGCCTC
ENED-R	CATTCAAGCAGCACTTCTGT
GM12824-F	ATCCTCTCAATGGGCTCAAC
GM12824-R	TAGCTGGGATGTGTCATGGT
SMTNL2-F	CTGTTTGGAGAAGTGGGAGCA
SMTNL2-R	TTGAGTCGAAGGCATCAGG
Primers used for ChIP-seq validation	
Peak1-F	GGGTTAGGGTTAGGGTTAGGG
Peak1-R	CACAGAAAGTGGATGCTCACAG
Peak4-F	AACCCTAACCCCAACCCTAA
Peak4-R	GAGGCCAAGTCAGGTTCATC
Peak9-F	TGCACGGATAGAAAGGGAAA

Peak9-R	TTGTTCTCACTCTGCCACCA
Peak14-F	ACCCAAGAGCACTCAAGGAA
Peak14-R	AGACCCAGCAGAAGGATGG
Peak27-F	CGGAAATGCTTCTGAGGAGA
Peak27-R	GTTTATTGGCGGGTCTAGG
Peak41-F	CTGGAGAAATACCCCAGCAG
Peak41-R	TTATGTGTTGTGGGGTACA
Peak260-F	GCCATTCCATGCTAGTCAT
Peak260-R	AGCCATCTCACCAAGCCCTAT
Peak561-F	TCTCTCCAGCCCTTCATCTG
Peak561-R	TACTGTGGCTTCCCCCTCA
Peak707-F	TGAATGCCAAGGCTTCTACA
Peak707-R	TGCAAATTCCACATACACAAAA
Peak764-F	GCAACCTTGCTCAGGTGACT
Peak764-R	GAGGTGCCGACTAGAGATGC
Peak841-F	CACCCATTGTGCTCCTTGTA
Peak841-R	GGACTCCGTCACCTGAGCTA
Peak2675-F	TGGCTGTAAAAGCATGAGCA
Peak2675-R	CCTGGCCAGCTTCTGAAGTA
Peak8218-F	ATTCAGGCCCAAGTGCATA
Peak8218-R	TGCTTGGCCTGGAAACTTTA
Peak29521-F	GCACCCATCACCTCTTCCT
Peak29521-R	TGAACTAGAACATGCGTTGCTT
NC1-F	ACCAAATATGGGTCTCTGC
NC1-R	GGAAGAGGGTTAGGGTTAGGG
NC2-F	GTGGGCAATGAGGAAAGACA
NC2-R	TCTGTGCACAAAAATCAGCA
Primers used for cloning of Rap1 DNA binding fragments	
CTGF-xhol-F	TACCCTCGAGATTCTGCTCAGCATAAGACC
CTGF-HindIII-R	AGCAAAGCTTCTCTTACTTGCAGTAGGACC
HIC1-xhol-F	ATGACTCGAGAGCCATGTCCTCAGACACATAG
HIC1-HindIII-R	ATAGAACGTTGATTATCTGGAGCTGGCATT
ANGPTL4-xhol-F	TTGTCTCGAGACACTTGACCAAGCTGGCCTT
ANGPTL4-HindIII-R	CTGCAAGCTTGAGCCATCTCACCAAGCCCTA